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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, circulating soluble factors, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-444. The polypeptides sequences are designated SEQ ID NO: 445-888. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is unknown or any of the four bases.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-444 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-444. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-444 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-444. The sequence information can be a segment of any one of SEQ ID NO: 1-444 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-444.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information are provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization

probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-444 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-444 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-444; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-444; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-444. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-444; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in SEQ ID NO: 445-888; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-444; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provide methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady

and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-444.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-444. The sequence information can be a segment of any one of SEQ ID NO: 1-444 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-444. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 500 amino acids, more preferably less than 200 amino acids more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) *Cytokine* 4(2): 134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) *Annu. Rev. Immunol.* 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-444; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 445-888; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 445-888. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotide sequences of SEQ ID NO: 1-444; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing as SEQ ID NO: 445-888; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 445-888. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding,

extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-444 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-444 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-444 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-444, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that

are selective for (i.e. specifically hybridize to) any one of the polynucleotides of the invention are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-444, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-444 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-444, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-444, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-444 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-444 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE NUCLEIC ACIDS

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-444, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO: 445-888 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-444 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-444), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of an mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-444). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-444 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 445-888 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-444 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-444 or (b)

polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 445-888 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 445-888 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 445-888.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 445-888.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference), the GeneAtlas software (Molecular Simulations Inc. (MSI), San Diego, CA) (Sanchez and Sali (1998) *Proc. Natl. Acad. Sci.*, 95, 13597-13602; Kitson DH et al, (2000) "Remote homology detection using structural modeling - an evaluation" Submitted; Fischer and Eisenberg (1996) *Protein Sci.* 5, 947-955), Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark), and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual,

Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein. In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprise one or more domains fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to

avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be

inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both

upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as

an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin

9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998))

or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies

resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g.,

HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by *in vivo* animal models such as the cumulative contact enhancement test (Lastbom et al., *Toxicology* 125: 59-66, 1998), skin prick test (Hoffmann et al., *Allergy* 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., *Arch. Toxicol.* 73: 501-9), and murine local lymph node assay (Kimber et al., *J. Toxicol. Environ. Health* 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be

demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis,

systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bowman et al., *J. Virology* 61:1992-1998; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry*

13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zama et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et al., *Cellular Immunology* 155:111-122, 1994; Galy et al., *Blood* 85:2770-2778, 1995; Toki et al., *Proc. Nat. Acad. Sci. USA* 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils,

T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al. *APMIS* 103:140-146, 1995; Muller et al. *Eur. J. Immunol.* 25:1744-1748; Gruber et al. *J. of Immunol.* 152:5860-5867, 1994; Johnston et al. *J. of Immunol.* 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., *J. Clin. Pharmacol.* 26:131-140, 1986; Burdick et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey et al., *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically

effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available,

e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent

molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see

Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol.*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem.*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligand(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myleogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia,

acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome),

poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, *Science*, 219:56, or by B. Waksman et al., 1963, *Int. Arch. Allergy Appl. Immunol.*, 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed *Mycobacterium tuberculosis* in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed *Mycobacterium tuberculosis* in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of *Mycobacterium* CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound

would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents,

fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered

alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue; often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within

the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition,

stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide

antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable

form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on

total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount

effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} . Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' , and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence

of the full length protein, such as the amino acid sequences shown in SEQ ID NO: 445-888, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

4.13.1 POLYCLONAL ANTIBODIES

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to

a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (*The Scientist*, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

4.13.2 MONOCLONAL ANTIBODIES

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro. The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are

desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for

example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, *Nature* **368**, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

4.13.3 HUMANIZED ANTIBODIES

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., *Nature*, **321**:522-525 (1986); Riechmann et al., *Nature*, **332**:323-327 (1988); Verhoeyen et al., *Science*, **239**:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable

domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

4.13.4 HUMAN ANTIBODIES

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host

have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

4.13.5 F_{ab} FRAGMENTS AND SINGLE CHAIN ANTIBODIES

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

4.13.6 BISPECIFIC ANTIBODIES

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab' -TNB derivatives is then reconverted to the Fab' -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab' -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology

described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

4.13.7 HETEROCONJUGATE ANTIBODIES

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

4.13.8 EFFECTOR FUNCTION ENGINEERING

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-444 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-444 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer

readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments,

such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers

that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic

or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-444, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting

the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., *Application of Synthetic Peptides: Antisense Peptides*, "In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., *Biochemistry* 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-444. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-444 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides

additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include *in situ* hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent *in situ* hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) *Human Chromosomes: A Manual of Basic Techniques*, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) *J. Clin. Microbiol.* 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) *Mol. Cell*

Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ μ l) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. The single-stranded DNA solution is then dispensed into CovaLink NH strips (75 μ l/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 μ l added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) *Science* 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) *Nucleic Acids Res.* 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) *Anal. Biochem.* 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) *PNAS USA* 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples

may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviJI*, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 μ g instead of 2-5 μ g); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5. EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences

5.2 EXAMPLE 2

Assemblage of Novel Nucleic Acids

The nucleic acids of the present invention, designated as SEQ ID NO: 1-444 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST, gb pri, and UniGene, and exons from public domain genomic sequences predicated by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), full-length gene sequences and their corresponding protein sequences were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTXY algorithm against Genbank (i.e., dbEST, gb pri, UniGene, and Genpept). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences are shown in the Sequence Listing as SEQ ID NO: 1-444. The corresponding polypeptide sequences are SEQ ID NO: 445-888.

Table 1 shows the various tissue sources of SEQ ID NO: 1-444.

The nearest neighbor results for polypeptides encoded by SEQ ID NO: 1-444 (i.e. SEQ ID NO: 445-888) were obtained by a BLASTP (version 2.0a1 19MP-WashU) search against Genpept release 124 using BLAST algorithm. The nearest neighbor result showed the closest homologue with functional annotation for SEQ ID NO: 1-444 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1-444 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), polypeptides encoded by SEQ ID NO: 1-444 (i.e. SEQ ID NO: 445-888) were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) polypeptides encoded by SEQ ID NO: 1-444 (i.e. SEQ ID NO: 445-888) were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The GeneAtlas™ software package (Molecular Simulations Inc. (MSI), San Diego, CA) was used to predict the three-dimensional structure models for the polypeptides encoded by SEQ ID NO: 1-444 (i.e. SEQ ID NO: 445-888). Models were generated by (1) PSI-BLAST which is a multiple alignment sequence profile-based searching developed by Altschul et al, (Nucl. Acids. Res. 25, 3389-3408 (1997)), (2) High Throughput Modeling (HTM) (Molecular Simulations Inc. (MSI) San Diego, CA,) which is an automated sequence and structure searching procedure (<http://www.msi.com/>), and (3) SeqFold™ which is a fold recognition method described by Fischer and Eisenberg (J. Mol. Biol. 209, 779-791 (1998)). This analysis was carried out, in part, by comparing the polypeptides of the invention with the known NMR (nuclear magnetic resonance) and x-ray crystal three-dimensional structures as templates. Table 5 shows, "PDB ID", the Protein DataBase (PDB) identifier given to template structure; "Chain ID", identifier of the subcomponent of the PDB template structure; "Compound Information", information of the PDB template structure and/or its subcomponents; "PDB Function Annotation" gives function of the PDB template as annotated by the PDB files (<http://www.rcsb.org/PDB/>); start and end amino acid position of the protein sequence aligned; PSI-BLAST score, the verify score, the SeqFold score, and the Potential(s) of Mean Force (PMF). The verify score is produced by GeneAtlas™

software (MSI), is based on Dr. Eisenberg's Profile-3D threading program developed in Dr. David Eisenberg's laboratory (US patent no. 5,436,850 and Luthy, Bowie, and Eisenberg, Nature, 356:83-85 (1992)) and a publication by R. Sanchez and A. Sali, Proc. Natl. Acad. Sci. USA, 95:13597-12502. The verify score produced by GeneAtlas normalizes the verify score for proteins with different lengths so that a unified cutoff can be used to select good models as follows:

$$\text{Verify score (normalized)} = (\text{raw score} - 1/2 \text{ high score}) / (1/2 \text{ high score})$$

The PFM score, produced by GeneAtlas™ software (MSI), is a composite scoring function that depends in part on the compactness of the model, sequence identity in the alignment used to build the model, pairwise and surface mean force potentials (MFP). As given in table 8, a verify score between 0 to 1.0, with 1 being the best, represents a good model. Similarly, a PMF score between 0 to 1.0, with 1 being the best, represents a good model. A SeqFold™ score of more than 50 is considered significant. A good model may also be determined by one of skill in the art based all the information in Table 5 taken in totality.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determined from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et al, as reference, were obtained for the polypeptide sequences. Table 6 shows the position of the last amino acid of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 7 correlates each of SEQ ID NO: 1-444 to a specific chromosomal location.

Table 8 is a correlation table of the novel polynucleotide sequences SEQ ID NO: 1-444, and their corresponding priority nucleotide sequences in the priority application USSN 09/659,671, herein incorporated by reference in its entirety.

TABLE 1

Tissue Origin	RNA Source	Library Name	SEQ ID NO:
adult brain	GIBCO	AB3001	4 6-8 12 23 33-34 47 50 55 57-60 62 89 102 104-106 123 144 162 176-177 179 187 194 248 260 270 279 292 294 297-298 307 322- 323 326 333 336 341 351 450
adult brain	GIBCO	ABD003	6 10 12-15 17-18 26 31 34-35 38-40 42-44 46 48-50 53 56 59-60 64 66 70-72 80-81 85-86 98 101 107 116-117 125 130 138-139 142 144 147 151 160-161 164 173 175-177 179 184-185 187-188 194-195 198 201 215 217-218 222 226 228 232 239-240 243-244 247 252 256 258 260 264-265 267 274-275 284 288 290 293 298 306-308 314-315 318- 320 325-326 333-334 337 341 343 345-346 351-354 364-365 371 390-391 424-425 429
adult brain	Clontech	ABR001	5 36 43 76 108 128 182-183 212 239 242 260 263 269 296 325 351 364 371-372 423
adult brain	Clontech	ABR006	2 9 11 13 18 23 35 38 42 46 50-51 53-54 60 63 66 85 91 107-108 116-117 120 122 128 170 178 180 184 187-188 193-194 198 202 215 232 243 245 257-258 260 266-267 271 285 294 301 333-334 337 370 389 394-396 400 405 412 423 428 434 436 453 458
adult brain	Clontech	ABR008	1 3 7 10-14 16-17 19-23 26-28 34-35 38-39 41 43 46-48 51-54 56 60 62 64 66-68 75 82 86-87 91 96-98 102 104-106 108 110-111 114 116-118 122 125 127-130 134 138-139 141-143 145-146 150-151 153 156 158 160 162 167-170 173-175 177-180 182 185-186 191-194 196-197 200-201 205-206 208-209 211 213-215 219-220 226-227 231 238 241 244 246-248 252 256 260 262-265 269 271 273 278-280 282 284 290 292 296 298 301- 302 306 309 311 315-317 322-323 325-327 329-331 335-337 339 342-343 345-346 350-355 359-360 362 364 368 370 372 374 376 381 383 385 387 390-395 400-401 405 410 412 414 417 420-421 423-425 432 440 447 450-452 459 472-473
adult brain	Clontech	ABR011	174 177 360
adult brain	BioChain	ABR012	334 341
adult brain	BioChain	ABR013	41-42 60 101 163 355
adult brain	Invitrogen	ABR014	53 95 104-106 143 149 177 180 258
adult brain	Invitrogen	ABR015	42 70-72 79 95 112 138-140 163 195 275 288 322-323 341 343 458
adult brain	Invitrogen	ABR016	13 31 60 79 124 136 154 163 333 341 343 364 370
adult brain	Invitrogen	ABT004	1 11-13 15 18 24-26 34 50 56 68 87 98 104- 106 111 123-124 131-133 137 144 146 173 189 194 206 224 247-248 260 262 264 269 272 274 282 298 318 327 335 346 351 356- 357 372 375 381 392 409-410 421
cultured preadipocytes	Stratagene	ADP001	2 11-14 24-25 40 42 47 50 52 57-58 69 76 107 120 144 151 156 163 168 171 194 197 199 203-204 215 229 250-251 262 294 333 338 341 415 450 469-473
adrenal gland	Clontech	ADR002	10-11 16 18 22-23 27-28 33-35 40 43-45 49 61 66 85 98 107-108 111 116-117 124 136 143 145 160 167 173 175 184 187 201 217-

			218-229 249-251 258 262 269 271 273 277 280 287 289 298 301 308 322-323 337 352 354 360 414 425 445-446 463
adult heart	GIBCO	AHR001	11-13 15 20-23 26-27 30 33-34 37-40 49 53 56-58 62-65 67-68 76-77 81 86 88 93-94 101 104-108 112 114 116-117 119 121-125 128-130 142 144-145 148 150 154-156 164-165 167 174-176 178-179 182 184 186-187 189 195 198 200 202 210 213-219 221 228-229 235 238 240 242-243 246-247 252-253 260 262 264 266-267 269 275 278 280-281 283 286-289 293-294 297 302-304 308 311 313 315-316 318-320 322-324 328-331 333 336 340-341 343 347 355-356 359 380-382 386-388 413-414 436
adult kidney	GIBCO	AKD001	4-5 8-13 15-18 20-27 33-35 37 39 42 45-46 49 52-54 56-59 62 66-67 73 75 77 80-81 83 85-86 88 91 97-98 100-108 112 117 119 122 124-125 127-129 134 138-142 145-146 151 153 155 158 160 162 164-165 168 170 174-176 178-181 186-189 196-199 202 209 211-212 215-216 222 232 235 237-240 244 246-248 250-252 257-258 260 262 264 269-271 275 280 282-284 287-289 291-294 297 303-312 314-317 322-323 325 327-329 333 336-337 341 357 359 375 403 407-408 413 428 436 469-471
adult kidney	Invitrogen	AKT002	1 10-11 13 17-18 26-27 35 42 54 64 66 73 77 82 87 91 94 96-97 113-114 118 135 146 148 160 173-174 182 187 196 198 200 218- 219 221 239 243-244 249-251 257-258 260 264 269-270 274-275 284-285 287-288 290 302-303 308-309 312 322-324 330 332-333 335-337 344 346 369 402 404 417 425 428 447 462
adult lung	GIBCO	ALG001	4 6 17-18 24-26 39 43-44 46 49 51 53 55 57-58 76 84 90 95 98 107 111 126 150 155 157 164 173 176 184 187 195 210 248-249 252-253 261 264 275 278 281 287 306 309 312 314 322-323 333 338 340-341 352 358 365 372 403 450
lymph node	Clontech	ALN001	17 19 26 81 85 149 166 218 228 260 264 275-276 282 321 333 341 395-396 436
young liver	GIBCO	ALV001	10 12 14 16-18 20 22 33 40 46 48 56 73 82 85 88 100 102 117 126 134 142-143 173 175 182 197 209 220 237-239 243 246-247 279 290 294 302 306 309 319-320 327 334 359
adult liver	Invitrogen	ALV002	10 15 22 24-25 33 49 66 75 86 95 109 111 130 138-139 148 151 156 187 189 222 237- 238 246 249 274 282 286 290 298 301 333 371 377 387 395 424-425 430
adult liver	Clontech	ALV003	73 92 294 341
adult ovary	Invitrogen	AOV001	1 4 6-18 23 27-28 30-34 39 42-47 49-50 52- 59 61-62 64-68 75-77 79 81-82 85-88 90 93-96 98 100-107 109-111 113-115 117 121 123 125-129 134-136 140 142-145 148 151 154 156 158 160-164 169-171 175-176 178-179 181-184 187-188 194-196 200 202-204 206 209-210 212 214-215 217-220 222-224 227 229 233 235 238-240 242-244 246-253 256 259-260 262 264-265 267 269

			275 277-281 283-284 287-294 296-298 301-304 306-308 310-311 313-316 318-326 328-330 333-342 344 346 349 352-353 356-358 360-361 363 369 372 375 382-383 395-396 402-403 405-407 409 415 417-419 421 425-427 435-436 450 456 467 469-473
adult placenta	Invitrogen	APL001	17 33 157 228 232 264
placenta	Invitrogen	APL002	11-12 23 31 35 51 53 88 104-106 138-139 151 260 279 296 307 327 334 337
adult spleen	GIBCO	ASP001	1 5 11 14 18-20 22-23 33-34 39-40 48-49 56-59 62 65 87 91 95 98 104-106 108-109 113-115 124 128 142 145 149-150 158 162- 163 173 195 198 202 210 224 227 232 250- 251 253 264 275 277 281 285-286 299 321 333 399
adult testis	GIBCO	ATS001	8 10-11 13 17 28 43-44 49 54 57-59 62 77 109 134 138-139 143-144 148 156 163-164 174 178 182 187-188 200 202 206 216 221 232 243 258 290 292 294 297-298 304 308- 309 324 333 336-337 339-341 346 425 472- 473
adult bladder	Invitrogen	BLD001	11 24-25 44 57-58 65 141 150-151 163 187 195 222 224 244-245 247 260 263 277 282 334 356 369 375 390-391 416 425 472-473
bone marrow	Clontech	BMD001	9 11 13-14 17 19 22-23 27-28 30 32-35 38 42 46 48-49 51 56-58 62-63 68 74-76 78 80 84-85 87 89 91 93 95 97-98 102 104-106 108 111-112 114-115 117 121-122 125 138-140 143 146 149 151 154-155 157-171 174 176 179 184 187 190 195 200 202 205- 206 210 215 218-222 224-236 239 249 258 262 264 269 285 294 297 304 310 319-321 324-325 331 333 341-342 363 420 450
bone marrow	Clontech	BMD002	1 5 7 10-11 14 16 19-20 23-25 28 30-31 35 40 42-43 46 48-49 51 54 56 62 64 68 74 77 87 89 91 93-96 98-99 104-106 108 110 114-115 117 121-122 128 138-139 141 143 145-146 149-151 156-158 163 165 169-171 174 178-179 181 195 199 203-206 210 212 216 218 220-221 224 234-235 240 245 248- 252 254-255 258-260 262 264 269 276-278 285 292 302-303 308-309 312 322-324 326 333 341 343 346 350 352 355 362 379 384- 386 394 410 418 420 425 440-441 449-451 469-474
bone marrow	Clontech	BMD004	97 149
bone marrow	Clontech	BMD007	53 143 149 221
colon	Invitrogen	CLN001	10 34 49 52-53 57-59 145 163 175 197 238 246-247 315-316 346 364 442
mixture of 16 tissues/mRNAs	various vendors	CTL016	10 56
mixture of 16 tissues/mRNAs	various vendors	CTL021	149
mixture of 16 tissues/mRNAs	various vendors	CTL028	145 358
adult cervix	BioChain	CVX001	1 4 6 11 23-25 27 30 34-35 39-40 46 50 59 62-64 76-77 80-81 88 93 100 107 111-112 116 118-119 122-123 125 136 138-139 143 146 151 155 160 163 176 178-182 184 188 195 209 215 218 221 228 232-233 235 239- 240 250-251 261-262 264 266 278 283 287- 288 300 306-308 311 319-320 322-323 325

			329 333 337 341 349 361 369 388 397 403 407 422 425 429-430 435-436 453 469-471
endothelial cells	Stratagene	EDT001	1 4 6-8 10-14 16-28 31 34-35 37 39 42-44 46 49 51 53-54 56-59 62-63 66 70-72 76-78 80-81 83-84 88 96 101 104-107 110 114 116 118-119 122-124 130 134 136 138-140 143-146 153-155 158 160 162-163 170 174-175 184 186-187 189 194-195 197 200 203-204 209-210 212 214-217 219 222-223 229 232-233 235-238 240 242 244 246-248 250-251 253 256 258 260-262 264 267 269- 270 272 276-277 279-282 284-285 288-292 294 302-304 308 312 317 319-320 324-325 329 333-334 336-337 339 341 361 375 378 384-385 397 404 411 415-416 450 469-473
fetal brain	Clontech	FBR001	46 104-106 175 193 258 341
fetal brain	Clontech	FBR004	193-194 226-227 229 260 264 334
fetal brain	Clontech	FBR006	2-3 9-12 14 16-17 19-20 23 27-28 39 43 52- 53 59 66-67 76 86 91-92 94-95 97-98 101- 102 104-108 110-111 116-117 125 127-130 134 138-139 142-143 145-148 150-151 167 170 174-175 178-179 185 187 194 198 200- 201 212 215 226-228 231 241 245 261 264 269 276-277 279 281-282 284 290 292 300 302 309 325 327 331 333-334 336-337 345 350-353 357 362 371 376 382-383 388-389 392 395-396 399 401 414 420 427 432 453 456 458 472-473
fetal brain	Clontech	FBR003	199 291 402
fetal brain	Invitrogen	FBT002	12 15 19-20 23 30-31 47 53 59 76 86 94 99 104-107 128 131-133 136 144 148 150 163 168 173 175 185 201 220 233 244 250-251 254-255 262 273 282 307 309 315-316 322- 323 327 334-335 337 341 351 364 375 392 409-412 421 423 469-473
fetal heart	Invitrogen	FHR001	34 43 81 87 129 134 138-139 145 200 288- 289 304 315-316 392
fetal kidney	Clontech	FKD001	6 8 10 17 50 54 77 86 92 112 114 179 217 223 241 269 301 319-320 322-323 333 340- 341 397-398
fetal kidney	Clontech	FKD002	141 264 309 341 432
fetal kidney	Invitrogen	FKD007	107 123
fetal lung	Clontech	FLG001	16 33 92 100 149 257 337 340 396
fetal lung	Invitrogen	FLG003	8 13 15 32 39 48 51 56 91-93 130-133 146 148 197-198 222 244 257 262 280 286 294 302 315-316 327 337 352 364 392 396 440
fetal lung	Clontech	FLG004	122 209
fetal liver-spleen	Columbia University	FLS001	1-13 15-46 48-51 53 55 57-59 61-95 97-119 121-136 138-139 141 143 146-155 158 160 162-165 167 169-171 178 184 186-187 189 195 209 211-212 214 219-221 223 227-229 234-252 254-265 267-269 272-280 283 288 290-291 295-299 302 304 307 312-317 322-323 333 341 343-344 352-353 361 365-367 371 390-391 402 418 441 444 466 469-473
fetal liver-spleen	Columbia University	FLS002	1-3 5 11-13 15-18 20-22 24-25 27 29-31 33-34 36-40 43-44 46 49 51 53-54 56-59 61 63-65 67-68 73 75 77 80-81 84-86 88-90 92-95 97-98 100 103 107-109 111 114 119 121-122 124 126-127 129-134 138-139 141-146 149 151-153 157-160 162 164-165

			167 169-171 178-180 183 190 193 200 209-214 218-219 221-222 225 227 233-235 238-239 244 246-252 257-261 267 269 274-275 277 285 288 291 294 296 299 308 312 314-316 333-334 336 338 341-342 352-353 364-366 372 382 395-396 402-403 405 416 420 425 436 441 443 446 449 457 469-473
fetal liver-spleen	Columbia University	FLS003	1 3 19 40 49 54 57-59 68 73 83 92 100 104-106 170 176 183 256 260 279 304 314 386 398 427 467
fetal liver	Invitrogen	FLV001	2 10 14 18 20 26 35 66 92 124 143 146 151 174-175 186 197 200 209 224 238 244 246 258 278-279 282 309 333 366 377 400 408
fetal liver	Clontech	FLV002	92 126 244
fetal liver	Clontech	FLV004	34-35 48 51 53 92 104-106 110 128 141 146 149 151 160 249 292 333 338 341 359 421
fetal muscle	Invitrogen	FMS001	11-12 44 76 110-111 145 148-149 178 187 226 258 260 262 264-265 290 341-342 400-401 404 456
fetal muscle	Invitrogen	FMS002	8 11 23 46 52 61 102 111 120 130 134 148 150 170 226 233 292 318 334 355 365 386 414 418 475
fetal skin	Invitrogen	FSK001	5-6 8 10 12 23 26-29 32-33 40 42 48-50 53 55-56 59 64 67 69-72 76 83 88 98-99 102 110 113 117 123 127-128 131-133 138-139 143 148 160 163 167 174-175 195 209-210 220-221 223-224 227 237-238 240 244-247 254-255 257-258 262-263 269 277 280-282 288 290-291 294-295 298-299 307 309 322-323 327 330 333 336-337 340-341 346 361 364 375 387 404 408 428 432 434-435 443 448-449 452 454
fetal skin	Invitrogen	FSK002	9 14 22 34-35 39-40 56 73 104-106 109 142-143 150 160 211 220-221 235 240 249 259 270 302 330 431 448 450 460
fetal spleen	BioChain	FSP001	276
umbilical cord	BioChain	FUC001	4-6 8 11 13 16 18 21-25 27 32 35 37 39-40 42 45 54 61 63 65-66 68 82 88 92-94 97 100-101 103-106 123 128-129 136 138-139 143 154 160-161 163 167 176 179-180 188 195 218 220 224 232-233 237 240-241 244 247 249 262 267 277 280 284 288 291 294 297-299 306 314 325 329 333-335 339 341 345 350 352 362 365 369-370 390-391 396-397 416 472-473
fetal brain	GIBCO	HFB001	3-4 6 11 13-14 18-20 22-23 26-27 34 37 42 50 54-58 60 62-65 67 70-72 78 80-81 83-84 87 93 98 101-107 111-112 114 116 118 123 125 129 131-145 147 151 154 156 162-165 172-173 175-180 182-191 193-195 197-206 208-217 223 227 233 239-240 242-244 247 258-259 261 264 267 269 273 277 282 286 288 290 301-302 306 310 313 325 333-334 336-337 341 343 345 351 364 369-372 469-473
macrophage	Invitrogen	HMP001	49 123 144 151 275
infant brain	Columbia University	IB2002	7-8 11-13 16 20-22 24-26 34 38 44-58 60 62-64 66 68 75 80 84 87 91-92 94 97-98 101 103-108 123 126 128 130-133 135-137 142-146 148 151 156 158 160 164 170 173

			175 177-178 180 182 187-188 194 196-198 200-201 206 212 215 217 219 226 232-233 239 241 247-248 256 260 263 265 268 273 277-278 282-284 286 288-289 294 298 301-303 306-307 309 312 324 330 334-335 337-339 342-343 346-347 351 355 364 370 373-376 389-394 400 413 421 423-424 458 469-471
infant brain	Columbia University	IB2003	4 8 11 13-14 16 23 42 46-47 50 54 56-62 65-66 76 94 98 102 119-120 135 142-143 145 150-152 158 163-164 173 175 180 226 233 244 247 260 262 267 277 302 304 309 319-320 334-337 351 364 375 383 389-392 400 423 427 434 472-473
infant brain	Columbia University	IBM002	33 50 54 112 131-133 163 173 215 226 267 331 423
infant brain	Columbia University	IBS001	2 5 11 26 34 52 87 91 98 108 170 173 177 194 200-201 248 277 340 361 412 423
lung, fibroblast	Stratagene	LFB001	13 16-17 22 26 39 46 57-58 78 83 88 93 101 116 122 131-133 160 170 178 195 198 210 214 223 262 267 276 304 319-320 322- 323 333 341 349 375 383 417 447 455
lung tumor	Invitrogen	LGT002	10-12 15 17-18 20 23 26-28 30 32 34 37 39-40 43 49 51 56-58 62 64 66 80 85-87 91 94 98 101-102 104-106 108 111 122 124 126-129 134 136 142-144 147 156-157 168 173-176 179 184 186-187 189 195 197-198 203-204 209-210 218 220-222 226 232-233 237-239 244-246 249-251 253 257 259 269 273 277-279 282-284 287 300-301 308 310 314 319-320 327 333-335 341 346 348 352 358 362 369 371 377-379 392 394 397 406- 407 410 412 421-422 436 469-471
lymphocytes	ATCC	LPC001	7 10-11 14-15 18 20 24-25 27 33 35 43-44 49 57-58 65-66 74-75 80 88 95 103-106 108 113 116 124 130-133 145-146 151 163- 164 167-171 185 200 206 215 218 226 228 232 241 244 247-248 262 267 273 275-277 284 297 321 331 345 349 352 375 400 472- 473
leukocyte	GIBCO	LUC001	1 6-8 11 14-15 17-18 20 23-25 27-35 39 43 46 49 52-54 57-58 62-63 74 76-78 80-81 84-85 88 90 92-95 98 102 104-106 108 112 114 117 119 123-125 128 130-135 141 143- 146 148 151 153 156-158 160-164 166-168 171 174-176 178-179 181 183-184 187-188 195 199-200 202-204 206 209 211-216 218-219 221-223 226-228 232-235 239-240 242 244-245 247 256 258 260-262 264 266- 267 270 275-277 279-280 282 284-290 292-293 297-298 300-302 306 308-310 312 314 317-328 330 333 335 341 346 349 400 412 427 436-437 450 462 469-473
leukocyte	Clontech	LUC003	17 19 27 34 42-43 46 49 90 98 104-106 108 113 122-123 128 157 206 284-285 321 333 341 362 472-473
Melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	6 11 30 34 45 54-55 61-62 65-66 78 81 93 112 114 116 122 128 130 135 143 145 160 164 177 180 187 195 219 227 235 239-240 258 264-265 279-280 287 302 304 306 311 325 333 341 343 377 408 432
mammary gland	Invitrogen	MMG001	1 5 8 10-13 15-16 18 20 24-26 30-31 34 39-

			40 43 45 47 49-51 53-54 57-58 62 64 66 70-72 76 80 83 87-88 95-96 98-99 101-102 104-106 108-109 112 118 124-125 127-133 136 138-139 142-146 148 150-151 163 167 170-171 175 180 186-187 189 197 200 212 224 226-227 241 244 247-248 250-251 253-255 257-258 260 262-263 265 269 272 276-280 282-283 288 290 301 306-307 309 313 315-316 322-323 326-327 333-334 337 341 343-346 356 361 364 370 387 390-392 404 409 412 415 421 428 430-432 469-473
induced neuron cells	Stratagene	NTD001	7 20 42 47 49 53 83 121 134 136 151 153 195 202 218-219 223 247 264 267 269 302 312-313 339 382 427 444
retinoic acid-induced neuronal cells	Stratagene	NTR001	34 70-72 104-106 110 116 197 258 392 396 422
neuronal cells	Stratagene	NTU001	16 40 49 53-54 80 100 130 136 194 258 281 396 427 472-473
pituitary gland	Clontech	PIT004	54 119 170 200 242 264 270 319-320 333 336 341 414
placenta	Clontech	PLA003	32 304 341 421
prostate	Clontech	PRT001	9 13 21 23 53 59 79 83 88 119 123 127 160 162 178 180 182-183 187 209 250-251 273 278 292-293 306 329 333 336 409 442
rectum	Invitrogen	REC001	5 12 15 22 32 42 80 108 118 127 143-144 187 194 224 226 277 298 345 396 404 442 444
salivary gland	Clontech	SAL001	4 7 10 40 66 88 102 104-106 126 128 151 162 182 212 222 242 252 277 287 312 319- 320 348 369
salivary gland	Clontech	SALS03	42
skin fibroblast	ATCC	SFB001	54
skin fibroblast	ATCC	SFB003	87 144
small intestine	Clontech	SIN001	1 9 11 13 15 17-18 22 27 33 38 40 54 57-58 61 63-64 78-80 84 97 102 115-116 124 128-129 131-134 142 144 148 153 159-160 163 165 167 180 186 195 197-198 202-204 214-215 217 230 232 234 242-243 248 257 265 271 278 284 295 297 299 304 306 310- 311 319-321 328 333 337 341 358 372-373 395 408 438 461 467
skeletal muscle	Clontech	SKM001	13 64 76 87 92 104-106 122 176 202 302 322-323 327 341 451 464
skeletal muscle	Clontech	SKM002	246
skeletal muscle	Clontech	SKMS03	49
skeletal muscle	null	SKMS04	88
spinal cord	Clontech	SPC001	6 12 22-23 48 60 70-72 80 93 101-102 104- 106 114 125 135 138-139 143-144 148 162- 163 167 176 196 200 202-204 242-243 264 270 283 288 294 302 321 326 329 333 336 343 345 349 352 354 382 424-425 436 457
adult spleen	Clontech	SPLc01	2 98 120 141 164 166 244 260 278 394
stomach	Clontech	STO001	20 42 54 63 70-72 80-81 97 152 164 179 202 214 238 246 256 311 321 341 353 356 365 403-404 433
thalamus	Clontech	THA002	1 14 17 23 47 57-58 62 66 70-72 80 101 117 134 151 165 187 194 201 220 241 243 249 278 282 294 337 346 351 353-354 381 396 424 430 434
thymus	Clontech	THM001	11 33 39-40 44 49 63 73-74 90 102 108 128 135 149 157 161 164 166 176 194 219 240

			249 258-259 263-264 284 289 292 298 302 309 311 314 319-320 322-323 329 333 336 341 352 360 371 412 417 440 447 467 472- 473
thymus	Clontech	THMc02	9-10 15 17 24-25 27-28 34 38 40 43 49 57- 58 68 74 77 81 87 94-95 98 104-108 110 115-116 128 136-137 143 146 148-151 158 160 165 197 200 210-211 215 221-222 232 235 241 243 245 248 252 269 278 281 286 288-289 292 302 312 321 325 327 329 331 333 338 345 350 365 378 383 387 412 428 439-440 446 451-452 460 465 469-473
thyroid gland	Clontech	THR001	1 4-5 8-9 11-12 14-15 17 19 21-25 27 34 40 46 49 54-55 57-59 61-62 66-68 70-72 80-81 85 93 97-98 102-108 116 119 121-122 124 126-133 141-142 144 146 150-151 155 162-166 169 171 175-176 178-181 187-190 202-205 208 214-215 218-219 226 232 237-239 244 246-247 250-252 257-258 260 263-264 267 270-271 277 279 282-284 287-288 292 294 297 300 302-304 307-308 310-311 313 317 322-323 325 333 336-337 341 346 356 358 401 405-406 408-409 436 461
trachea	Clontech	TRC001	17 23 34 90 93 108 142 151 238 240 246 259 266 333 412 472-473
uterus	Clontech	UTR001	18 20 30-31 50 52 114 125 158 164 168 182 198 206 210 248 254-255 260 273 283 304 311 325 365 383 421 423

The 16 tissue/mRNAs and their vendor sources are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) Normal adult kidney mRNA (Invitrogen), 3) Normal fetal brain mRNA (Invitrogen), 4) Normal adult liver mRNA (Invitrogen), 5) Normal fetal kidney mRNA (Invitrogen), 6) Normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) Human bone marrow mRNA (Clontech), 10) Human leukemia lymphoblastic mRNA (Clontech), 11) Human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human so/spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

TABLE 2

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
445	gi4151328	Homo sapiens	high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.	2344	48
445	gi4151330	Homo sapiens	high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 beta mRNA, complete cds.	1694	59
445	gi2555183	Rattus norvegicus	SPA-1 like protein p1294	2324	48
446	gi13517972	Homo sapiens	PR-domain containing protein 17 mRNA, complete cds.	2496	100
446	gi10434545	Homo sapiens	cDNA FLJ12827 fis, clone NT2RP2002939, weakly similar to ZINC FINGER PROTEIN 136.	2496	100
446	gi13623607	Homo sapiens	, zinc finger protein 136 (clone pHZ-20), clone MGC:12711, mRNA, complete cds.	710	42
447	gi6093239	Homo sapiens	mRNA; cDNA DKFZp434O0515 (from clone DKFZp434O0515).	1054	100
447	gi3522970	Homo sapiens	Trio mRNA, complete cds.	216	23
447	AAW27227	Homo sapiens	Human TRIO phosphoprotein.	216	23
448	gi7022890	Homo sapiens	cDNA FLJ10700 fis, clone NT2RP3000665.	2838	96
448	gi10438668	Homo sapiens	cDNA: FLJ22327 fis, clone HRC05572.	1333	100
448	gi7020045	Homo sapiens	cDNA FLJ20140 fis, clone COL07182.	1074	79
449	gi6102903	Homo sapiens	mRNA; cDNA DKFZp566D244 (from clone DKFZp566D244); partial cds.	2601	99
449	gi10434000	Homo sapiens	cDNA FLJ12485 fis, clone NT2RM2000420.	1907	100
449	gi10437387	Homo sapiens	cDNA: FLJ21308 fis, clone COL02131.	1519	69
450	gi7670836	Homo sapiens	hepatocellular carcinoma-associated antigen 66 (HCA66) mRNA, complete cds.	3101	99
450	gi7959764	Homo sapiens	PRO1289	935	100
450	gi927708	Saccharomyces cerevisiae	Ydr449cp; CAI: 0.18	288	32
451	gi7020902	Homo sapiens	cDNA FLJ20657 fis, clone KAT01069.	3231	99
451	gi11037252	Rattus norvegicus	NPL4	3156	96
451	gi10434779	Homo sapiens	cDNA FLJ12984 fis, clone NT2RP3000047, weakly similar to NPL4 PROTEIN.	2812	99
452	gi13160469	Homo sapiens	WDR13 protein (WDR13) gene, complete cds.	1063	94
452	gi12044400	Homo sapiens	WDR13 protein (WDR13) mRNA, complete cds.	1063	94
452	gi13751862	Mus musculus	WD-repeat protein	1058	93
453	gi12619286	Homo sapiens	mRNA for spinal cord-derived protein FI58G, complete cds.	1133	100
453	gi7638241	Homo sapiens	mesenchymal stem cell protein DSC92 mRNA, complete cds.	1133	100
453	gi12804543	Homo sapiens	, mesenchymal stem cell protein DSC92, clone MGC:2824, mRNA, complete cds.	1133	100
454	gi13279287	Homo sapiens	, clone IMAGE:3633354, mRNA, partial cds.	2066	100
454	gi5052586	Drosophila melanogaster	BcDNA.GH08385	334	25
454	gi10433073	Homo sapiens	cDNA FLJ11749 fis, clone	190	26

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			HEMBA1005558, weakly similar to NUCLEAR PROTEIN SNF7.		
455	gi7019840	Homo sapiens	cDNA FLJ20018 fis, clone ADSE00909.	1698	99
455	gi13938166	Homo sapiens	, clone MGC:12617, mRNA, complete cds.	1630	98
455	gi9280376	Homo sapiens	ancient conserved domain protein 3 (ACDP3) mRNA, complete cds.	1271	90
456	gi7020190	Homo sapiens	cDNA FLJ20232 fis, clone COLF5593.	1487	100
456	gi14249896	Homo sapiens	, clone MGC:15774, mRNA, complete cds.	1479	99
456	gi9188416	Homo sapiens	Novel human gene mapping to chromosome 22.	1479	99
457	AAW75093	Homo sapiens	Human secreted protein encoded by gene 37 clone HFVGS85.	369	100
457	gi8895089	Homo sapiens	protein x 013 mRNA, complete cds.	145	41
457	gi14250569	Homo sapiens	, protein x 013, clone MGC:3073, mRNA, complete cds.	145	41
458	gi7020228	Homo sapiens	cDNA FLJ20257 fis, clone COLF7231.	1169	100
458	gi7528184	Drosophila melanogaster	bicoid-interacting protein BIN3	389	45
459	gi11345384	Homo sapiens	vacuolar protein sorting protein 18 (VPS18) mRNA, complete cds.	5102	100
459	AAW48303	Homo sapiens	Amino acid sequence of human deep orange protein.	2555	100
459	gi2832850	Drosophila melanogaster	EG:171E4.1	1316	35
460	gi6966967	Homo sapiens	mRNA for dipeptidyl-peptidase III (DPP3 gene).	3814	99
460	gi13938201	Homo sapiens	, dipeptidylpeptidase III, clone MGC:15061, mRNA, complete cds.	3811	99
460	AAB67571	Homo sapiens	Amino acid sequence of a human hydrolytic enzyme HYENZ3.	3807	99
461	AAV53020	Homo sapiens	Human secreted protein clone qb56_19 protein sequence SEQ ID NO:46.	657	100
461	AAV59788	Homo sapiens	Human normal ovarian tissue derived protein 65.	618	100
461	AAG04028	Homo sapiens	Human secreted protein, SEQ ID NO: 8109.	442	72
462	gi13021843	Homo sapiens	polyadenylate binding protein-interacting protein 2 mRNA, complete cds.	679	100
462	gi12052806	Homo sapiens	mRNA; cDNA DKFZp564F163 (from clone DKFZp564F163); complete cds.	675	99
462	gi7106826	Homo sapiens	HSPC218	673	99
463	gi7023258	Homo sapiens	cDNA FLJ10914 fis, clone OVARC1000212.	1067	100
464	gi7023258	Homo sapiens	cDNA FLJ10914 fis, clone OVARC1000212.	649	72
465	gi7022147	Homo sapiens	cDNA FLJ10233 fis, clone HEMBB1000266.	3464	100
465	gi12224837	Homo sapiens	mRNA; cDNA DKFZp547K202 (from clone DKFZp547K202).	3464	100
465	AAV99662	Homo sapiens	Human GTPase associated protein-13.	3464	100
466	gi7582304	Homo sapiens	BM-016	584	100
466	AAW85610	Homo sapiens	Secreted protein clone eh80_1.	330	97
466	AAW78199	Homo sapiens	Human secreted protein encoded by gene 74 clone HGBAC11.	330	97
467	gi7018410	Homo sapiens	mRNA; cDNA DKFZp566K023 (from clone DKFZp566K023).	1010	100
467	gi9049987	Rattus	X2CR1 protein	268	81

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
		norvegicus			
468	gi8317213	Homo sapiens	histone acetyltransferase (MOF) mRNA, partial cds.	1625	100
468	gi10433157	Homo sapiens	cDNA FLJ11810 fis, clone HEMBA1006347, moderately similar to MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).	1625	100
468	gi10436400	Homo sapiens	cDNA FLJ14040 fis, clone HEMBA1005513, weakly similar to MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).	1613	99
469	AAAY76072	Homo sapiens	Human skin cell protein, SEQ ID NO:327.	668	100
469	AAB56011	Homo sapiens	Skin cell protein, SEQ ID NO: 327.	668	100
470	gi29481	Homo sapiens	Human erythrocyte 2,3-bisphosphoglycerate mutase mRNA EC 2.7.5.4.	1362	100
470	gi179527	Homo sapiens	Human 2,3-bisphosphoglycerate mutase (BPGM) gene, exon 3.	1362	100
470	AAB11959	Homo sapiens	Glycated human erythrocyte bisphosphoglycerate mutase (BPGM).	1362	100
471	gi6841472	Homo sapiens	HSPC125	892	100
471	gi12001966	Homo sapiens	clone 015g09 My013 protein mRNA, complete cds.	892	100
471	gi9624483	Homo sapiens	HRPAP20 short form mRNA, complete cds.	640	72
472	gi9367763	Homo sapiens	mRNA for zinc finger protein Cezanne (CEZANNE gene).	2580	100
472	gi6102920	Homo sapiens	mRNA; cDNA DKFZp434H0717 (from clone DKFZp434H0717); partial cds.	2197	100
472	gi7332054	Caenorhabditis elegans	contains similarity to tumor necrosis factors	126	25
473	gi8489813	Homo sapiens	DJ963K23.2 mRNA, complete cds.	1255	100
473	AAB43861	Homo sapiens	Human cancer associated protein sequence SEQ ID NO:1306.	1255	100
473	gi9858803	Mus musculus	Zfp228	1090	91
474	gi7020223	Homo sapiens	cDNA FLJ20254 fis, clone COLF6926.	2278	100
474	AAAY25743	Homo sapiens	Human secreted protein encoded from gene 33.	917	100
474	AAAY76166	Homo sapiens	Human secreted protein encoded by gene 43.	724	94
475	gi14042066	Homo sapiens	cDNA FLJ14503 fis, clone NT2RM1000252, weakly similar to H.sapiens E-MAP-115 mRNA.	159	26
475	gi7270600	Arabidopsis thaliana	trichohyalin like protein	156	25
475	gi180195	Homo sapiens	Human aorta caldesmon mRNA, complete cds.	145	25
476	gi11066250	Homo sapiens	presenilins associated rhomboid-like protein (PARL) mRNA, complete cds.	2030	100
476	gi13177766	Homo sapiens	, Similar to presenilins associated rhomboid-like protein, clone MGC:4756, mRNA, complete cds.	1107	99
476	gi7959883	Homo sapiens	PRO2207	986	100
477	AAAY91941	Homo sapiens	Human chaperone protein 2 (HCHP-2).	1977	100
477	gi7019854	Homo sapiens	cDNA FLJ20027 fis, clone ADSE01901.	1965	99
477	gi6567172	Mus musculus	mDj10	1863	93
478	gi13937971	Homo sapiens	, Similar to RIKEN cDNA 1110005A23 gene, clone MGC:14726, mRNA,	1040	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			complete cds.		
478	gi13940310	Homo sapiens	HCC-1 gene.	1040	100
478	AAB36609	Homo sapiens	Human FLEXHT-31 protein sequence SEQ ID NO:31.	1040	100
479	gi11065999	Homo sapiens	neuronal calcium binding protein NECAB3 mRNA, complete cds.	1889	99
479	gi10798741	Homo sapiens	XB51 mRNA for X11L-binding protein 51, complete cds.	654	99
479	gi10798743	Mus musculus	X11L binding protein 51	1079	86
480	gi6094684	Homo sapiens	PAC clone RP1-278D1 from X, complete sequence.	3056	92
480	gi10435614	Homo sapiens	cDNA FLJ13568 fis, clone PLACE1008368, weakly similar to RING CANAL PROTEIN.	1847	100
480	gi7023516	Homo sapiens	cDNA FLJ11078 fis, clone PLACE1005102, weakly similar to RING CANAL PROTEIN.	1208	42
481	gi7020424	Homo sapiens	cDNA FLJ20369 fis, clone HEP19364.	2727	100
481	gi1110599	Mus sp.	semaphorin homolog=M-Sema F	2653	86
481	AAB88485	Homo sapiens	Human membrane or secretory protein clone PSEC0078.	1774	100
482	gi4679028	Homo sapiens	HSPC021	1930	100
482	gi5106781	Homo sapiens	HSPC025	1930	100
482	gi12654535	Homo sapiens	, HSPC025, clone MGC:735, mRNA, complete cds.	1930	100
483	gi1145789	Rattus norvegicus	neuregulin 2	4417	98
483	gi7960135	Homo sapiens	neuregulin 3 isoform gene; complete cds, alternatively spliced.	2736	65
483	gi7960131	Homo sapiens	neuregulin 3 isoform HNL3 mRNA, complete cds, alternatively spliced.	2729	65
484	gi14250554	Homo sapiens	, hexokinase 1, clone MGC:1724, mRNA, complete cds.	4725	99
484	gi2873349	Homo sapiens	hexokinase I (HK1) gene, exon 18, complete cds, alternatively spliced.	4725	99
484	gi184021	Homo sapiens	Human hexokinase I (HK1) mRNA, complete cds.	4718	99
485	gi8453103	Homo sapiens	zinc finger protein mRNA, complete cds.	3726	100
485	gi13752754	Homo sapiens	zinc finger 1111 mRNA, complete cds.	1689	56
485	gi10436789	Homo sapiens	cDNA FLJ14345 fis, clone THYRO1001189, weakly similar to ZINC FINGER PROTEIN 91.	1683	56
486	AAB56937	Homo sapiens	Human prostate cancer antigen protein sequence SEQ ID NO:1515.	2341	100
486	gi12804453	Homo sapiens	, Similar to Tu translation elongation factor, mitochondrial, clone MGC:1592, mRNA, complete cds.	2326	100
486	gi899285	Homo sapiens	H.sapiens mRNA for elongations factor Tu-mitochondrial.	2326	100
487	gi9910111	Homo sapiens	myosin X (MYO10) mRNA, complete cds.	10727	99
487	gi6996558	Mus musculus	myosin X	10089	93
487	gi7108753	Homo sapiens	myosin X (MYO10) mRNA, partial cds.	8029	99
488	gi7688687	Homo sapiens	AD-017 protein mRNA, complete cds.	1935	100
488	gi14042251	Homo sapiens	cDNA FLJ14611 fis, clone NT2RP1000988.	1935	100
488	AAY66671	Homo sapiens	Membrane-bound protein PRO1134.	1935	100
489	gi202215	Mus musculus	alpha-tubulin isotype M-alpha-6	2387	100
489	gi14328047	Homo sapiens	, tubulin alpha 4, clone MGC:2379,	2387	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			mRNA, complete cds.		
489	gi1333692	Macaca fascicularis	alpha-tubulin (ATG-initiation codon missing)	2382	100
490	gi5912034	Homo sapiens	mRNA; cDNA DKFZp434N0535 (from clone DKFZp434N0535); partial cds.	6810	99
490	gi5912239	Homo sapiens	mRNA; cDNA DKFZp434O225 (from clone DKFZp434O225); partial cds.	3442	99
490	gi3292939	Drosophila melanogaster	Additional sex combs	295	39
491	gi5912034	Homo sapiens	mRNA; cDNA DKFZp434N0535 (from clone DKFZp434N0535); partial cds.	5941	99
491	gi5912239	Homo sapiens	mRNA; cDNA DKFZp434O225 (from clone DKFZp434O225); partial cds.	2573	99
491	gi3292939	Drosophila melanogaster	Additional sex combs	295	39
492	AAV68778	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-10.	2463	99
492	gi479173	Homo sapiens	H.sapiens nek3 mRNA for protein kinase.	2417	99
492	gi13529320	Mus musculus	Similar to NIMA (never in mitosis gene a)-related expressed kinase 3	1887	73
493	gi13539686	Homo sapiens	protein kinase C and casein kinase substrate 1 (PACSLN1) mRNA, complete cds.	2365	100
493	gi728604	Mus musculus	PACSLN	2250	95
493	gi4324452	Rattus norvegicus	syndapin I	2250	95
494	gi7023749	Homo sapiens	cDNA FLJ11220 fis, clone PLACE1008129.	3994	100
494	gi10433501	Homo sapiens	cDNA FLJ12104 fis, clone HEMBB1002697.	2829	100
494	gi5788108	Homo sapiens	PAC clone RP5-1087M19 from 7q11.23-q21.1, complete sequence.	757	63
495	AAB54375	Homo sapiens	Human pancreatic cancer antigen protein sequence SEQ ID NO:827.	2897	99
495	AAV57923	Homo sapiens	Human transmembrane protein HTPMN-47.	2724	98
495	AAW88628	Homo sapiens	Secreted protein encoded by gene 95 clone HPWAN23.	2686	98
496	gi7959788	Homo sapiens	PRO1635	317	100
496	AAW74852	Homo sapiens	Human secreted protein encoded by gene 124 clone HPCAD23.	143	100
497	gi7707424	Homo sapiens	mRNA for syntaxin 18, complete cds.	1705	100
498	gi1613858	Homo sapiens	Human zinc finger protein zfp47 (zf47) mRNA, partial cds.	1488	83
498	gi13938633	Mus musculus	RIKEN cDNA 2810435N07 gene	1318	60
498	gi9837564	Mus musculus	SCAN-KRAB-zinc finger protein	1242	58
499	AAV27795	Homo sapiens	Human secreted protein encoded by gene No. 79.	1539	99
499	gi10436317	Homo sapiens	cDNA FLJ13986 fis, clone Y79AA1001923, weakly similar to Homo sapiens F-box protein Fbx22 (FBX22) gene.	1370	100
499	gi6164747	Homo sapiens	F-box protein Fbx22 (FBX22) gene, partial cds.	391	93
500	gi3150052	Homo sapiens	TGF beta receptor associated protein-1 mRNA, complete cds.	4455	100
500	gi14280050	Homo sapiens	Vps39/Vam6-like protein gene, complete cds.	382	24
500	gi12718237	Neurospora	related to TGF beta receptor associated	174	31

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
		crassa	protein 1		
501	gi7023051	Homo sapiens	cDNA FLJ10796 fis, clone NT2RP4000648, weakly similar to TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.	3360	99
501	gi9651170	Homo sapiens	cell cycle checkpoint protein CHFR mRNA, complete cds.	2491	96
501	AAB20219	Homo sapiens	Human Chfr (checkpoint with FHA and ring finger) protein.	2491	96
502	gi7329074	Homo sapiens	collagen type V alpha 3 chain (COL5A3) mRNA, complete cds.	9671	100
502	gi8568094	Rattus norvegicus	alpha 4 type V collagen	8038	82
502	gi7329072	Mus musculus	collagen type V alpha 3 chain	7970	82
503	gi12654687	Homo sapiens	, clone MGC:2616, mRNA, complete cds.	1161	100
503	gi7769617	Mus musculus	TCE2	1050	89
504	gi12654687	Homo sapiens	, clone MGC:2616, mRNA, complete cds.	1140	96
504	gi7769617	Mus musculus	TCE2	1029	86
505	gi12654687	Homo sapiens	, clone MGC:2616, mRNA, complete cds.	654	100
505	gi7769617	Mus musculus	TCE2	629	92
506	gi14249942	Homo sapiens	, Similar to RIKEN cDNA 0610008P16 gene, clone MGC:15937, mRNA, complete cds.	1609	100
506	AAB56487	Homo sapiens	Human prostate cancer antigen protein sequence SEQ ID NO:1065.	1167	98
506	gi2828262	Bos taurus	aralkyl acyl-CoA:amino acid N-acyltransferase	597	40
507	gi7688987	Homo sapiens	uncharacterized bone marrow protein BM046	1295	100
507	AAB64387	Homo sapiens	Amino acid sequence of human intracellular signalling molecule INTRA19.	1202	94
507	gi9437511	Homo sapiens	BM024	1045	98
508	AAB18979	Homo sapiens	Amino acid sequence of a human transmembrane protein.	1203	100
508	gi6808196	Homo sapiens	mRNA; cDNA DKFZp434P1018 (from clone DKFZp434P1018); partial cds.	938	100
508	gi13960126	Homo sapiens	, Similar to leucine-rich neuronal protein, clone MGC:4126, mRNA, complete cds.	845	100
509	gi13938527	Homo sapiens	, Similar to RIKEN cDNA 2810002N01 gene, clone MGC:2562, mRNA, complete cds.	1048	100
509	AA Y35994	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 379.	1032	98
509	AAG00345	Homo sapiens	Human secreted protein, SEQ ID NO: 4426.	619	98
510	gi773387	Neurospora crassa	Restriction enzyme inactivation of met-10 complementation in this region. Sequence similarity to S. cerevisiae chromosome VIII cosmid 9205, accession no. U10556 CDS residues 22627-24126	536	35
510	gi487945	Saccharomyces cerevisiae	Yhr070wp	528	49
510	AAG02508	Homo sapiens	Human secreted protein, SEQ ID NO: 6589.	324	100
511	gi11493195	Homo sapiens	mRNA for LB1 protein.	2614	99
511	gi10434688	Homo sapiens	cDNA FLJ12920 fis, clone NT2RP2004594.	2604	99
511	gi12053201	Homo sapiens	mRNA; cDNA DKFZp434A1031 (from	2604	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			clone DKFZp434A1031); complete cds.		
512	AAW75106	Homo sapiens	Human secreted protein encoded by gene 50 clone HHSDZ57.	471	100
512	AAY59689	Homo sapiens	Secreted protein 26-44-1-B5-CL3 1.	471	100
512	AAY48331	Homo sapiens	Human prostate cancer-associated protein 28.	471	100
514	AAW67888	Homo sapiens	Human secreted protein encoded by gene 82 clone HSKHL65.	921	92
514	gi13436110	Homo sapiens	, Similar to RIKEN cDNA 2310034L04 gene, clone MGC:11061, mRNA, complete cds.	150	28
514	AAY53052	Homo sapiens	Human secreted protein clone df202_3 protein sequence SEQ ID NO:110.	132	33
515	gi7020259	Homo sapiens	cDNA FLJ20276 fis, clone HEP02437.	5378	100
515	gi10432807	Homo sapiens	cDNA FLJ11534 fis, clone HEMBA1002679.	3024	99
515	gi9916	Plasmodium falciparum	liver stage antigen	399	23
516	AAB67448	Homo sapiens	Amino acid sequence of a human chaperone polypeptide.	1190	99
516	gi13477189	Homo sapiens	, Similar to RIKEN cDNA 1300007M11 gene, clone MGC:12943, mRNA, complete cds.	1182	99
516	AAG03527	Homo sapiens	Human secreted protein, SEQ ID NO: 7608.	389	98
517	gi7023782	Homo sapiens	cDNA FLJ11240 fis, clone PLACE1008568.	2796	100
517	AAB08869	Homo sapiens	Amino acid sequence of a human secretory protein.	2792	99
517.	AAB23626	Homo sapiens	Human secreted protein SEQ ID NO: 52.	2792	99
518	gi6460009	Deinococcus radiodurans	citrate lyase, beta subunit	211	30
518	gi14025765	Mesorhizobium loti	citrate lyase beta-subunit	324	31
518	gi14024477	Mesorhizobium loti	Citrate lyase beta chain (acyl lyase subunit); CitE	316	33
519	gi14041831	Homo sapiens	cDNA FLJ14357 fis, clone HEMBA1000005, highly similar to DNAJ PROTEIN HOMOLOG MTJ1.	2873	100
519	AAB67447	Homo sapiens	Amino acid sequence of a human chaperone polypeptide.	2481	99
519	gi473847	Mus musculus	dnaJ-like protein	2413	84
520	gi7669968	Homo sapiens	mRNA; cDNA DKFZp761G0313 (from clone DKFZp761G0313).	789	100
520	gi4586315	Homo sapiens	ORCTL3 mRNA for organic-cation transporter like 3, complete cds.	348	38
520	gi4835384	Homo sapiens	DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds).	348	38
521	gi7959805	Homo sapiens	PRO0823	344	100
522	gi10434341	Homo sapiens	cDNA FLJ12691 fis, clone NT2RM4002571, weakly similar to H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).	2605	89
522	gi10436305	Homo sapiens	cDNA FLJ13977 fis, clone Y79AA1001603, weakly similar to POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41).	1631	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
522	gi971461	Homo sapiens	H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).	1386	50
523	gil1493500	Homo sapiens	PRO2979	477	100
523	gi38163	Pan troglodytes	A-gamma-globin	477	100
523	gi176779	Pan troglodytes	gamma-2 globin	477	100
524	gi5262582	Homo sapiens	mRNA; cDNA DKFZp434K063 (from clone DKFZp434K063); partial cds.	3782	99
524	gi10438230	Homo sapiens	cDNA: FLJ21993 fis, clone HEP06576.	1416	100
524	AAV21842	Homo sapiens	Human signal peptide-containing protein (SIGP) (clone ID 1273453).	1416	100
525	gi1928886	Rattus norvegicus	lin-10 protein homolog	2199	97
525	gi10433467	Homo sapiens	cDNA FLJ12076 fis, clone HEMBB1002442, weakly similar to LIN-10 PROTEIN.	483	98
525	gi5824587	Caenorhabditis elegans	T01G9.2b	668	37
526	gi1679607	Mus musculus	myosin-I	4206	84
526	gi1924940	Homo sapiens	H.sapiens mRNA for myosin-IE.	4115	99
526	gi65324	Gallus gallus	brush border myosin IB	3812	76
527	AAB63419	Homo sapiens	Human breast cancer associated antigen protein sequence SEQ ID NO:781.	641	99
528	gi13649967	Homo sapiens	fovea-associated SH3 domain binding protein (FASH3) mRNA, complete cds.	558	100
528	gi13539561	Homo sapiens	mRNA for SH3BGR12 protein.	558	100
528	gi5042302	Mus musculus	sh3bgr protein	365	64
529	gi10436540	Homo sapiens	cDNA FLJ14154 fis, clone NT2RM1000341.	1151	99
529	gi13436011	Mus musculus	RIKEN cDNA 1200013P24 gene	1139	97
529	gi1592161	Methanococcus jannaschii	ribosomal protein S18 alanine acetyltransferase	109	36
530	gi3135314	Homo sapiens	chromosome 7q22 sequence, complete sequence.	911	100
530	gi6752287	Homo sapiens	Novel human gene mapping to chromosome X.	281	51
531	gi14042818	Homo sapiens	cDNA FLJ14937 fis, clone PLACE1010231, weakly similar to CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR.	2548	97
531	gi2117161	Homo sapiens	H.sapiens mRNA for HE6 Tm7 receptor.	1366	52
531	AAW36903	Homo sapiens	Human epididymis-specific receptor protein.	1366	52
532	gi7417372	Homo sapiens	intracellular hyaluronan-binding protein mRNA, complete cds.	2175	99
532	gi7110497	Mus musculus	intracellular hyaluronan-binding protein p57	1862	85
532	gi3403154	Homo sapiens	Human Ki-1/57 intracellular antigen mRNA, partial cds.	1591	98
533	gi10436645	Homo sapiens	cDNA FLJ14235 fis, clone NT2RP4000167.	1585	82
533	gi7020976	Homo sapiens	cDNA FLJ20707 fis, clone KAIA1223.	2195	84
533	gi13276619	Homo sapiens	mRNA; cDNA DKFZp761I0112 (from clone DKFZp761I0112).	1444	99
534	gi438880	Rattus norvegicus	tropomyosin	1186	99
534	gi2978558	Xenopus	alpha-tropomyosin	1089	89

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
		laevis			
534	gi438882	Rattus norvegicus	tropomyosin	1086	92
535	gi438880	Rattus norvegicus	tropomyosin	1120	93
535	gi9508585	Homo sapiens	tropomyosin isoform mRNA, complete cds.	1105	93
535	gi12653955	Homo sapiens	, Similar to tropomyosin 4, clone MGC:3261, mRNA, complete cds.	1094	91
536	gi6808111	Homo sapiens	mRNA; cDNA DKFZp434O1230 (from clone DKFZp434O1230); partial cds.	439	100
537	gi6807806	Homo sapiens	mRNA; cDNA DKFZp434K031 (from clone DKFZp434K031); partial cds.	3007	100
537	gi13623334	Homo sapiens	, Similar to DKFZP727C091 protein, clone MGC:10677, mRNA, complete cds.	2392	100
537	AA25821	Homo sapiens	Human secreted protein fragment encoded from gene 41.	1967	99
538	AAB88413	Homo sapiens	Human membrane or secretory protein clone PSEC0170.	1818	99
538	gi6457342	Homo sapiens	E2IG4 (E2IG4) mRNA, complete cds.	1813	99
538	AAB24026	Homo sapiens	Human PRO1788 protein sequence SEQ IDNO:18.	1813	99
539	gi6572289	Homo sapiens	mRNA for mitochondrial tryptophanyl-tRNA synthetase (WARS2 gene).	1820	100
539	gi13421159	Caulobacter crescentus	tryptophanyl-tRNA synthetase	727	46
539	gi11992026	Zymomonas mobilis	tryptophanyl-tRNA synthase	721	43
540	gi7106630	Homo sapiens	Novel human mRNA from chromosome 1, clone Z98884, has homology to PERIOD CIRCADIAN PROTEIN 3.	6301	99
540	gi13160925	Homo sapiens	mRNA for period (Drosophila) homolog 3 hPER3, complete cds.	6274	99
540	AAB23266	Homo sapiens	Human circadian rhythm protein Per3 (hPer3).	6274	99
541	gi9621744	Homo sapiens	ferritin heavy chain subunit mRNA, complete cds.	968	100
541	gi12654093	Homo sapiens	, ferritin, heavy polypeptide 1, clone MGC:5580, mRNA, complete cds.	968	100
541	gi12655095	Homo sapiens	, ferritin, heavy polypeptide 1, clone MGC:1749, mRNA, complete cds.	968	100
542	gi4902699	Homo sapiens	Novel human gene mapping to chromosome 13.	2372	57
542	gi2341020	Homo sapiens	PAC clone 248O15 from 13q12-q13, complete sequence.	1447	58
542	gi11907986	Drosophila melanogaster	fry	1054	38
543	gi7582278	Homo sapiens	BM-003	1386	100
543	gi7688983	Homo sapiens	uncharacterized bone marrow protein BM044	1386	100
543	gi1752736	Saccharomyces cerevisiae	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w	150	35
544	gi1628401	Homo sapiens	H.sapiens mRNA for leucine-rich primary response protein 1.	3936	98
544	gi940821	Rattus norvegicus	LRPR1	2914	73
544	gi2196560	Schizosaccharomyces pombe	Mis6	223	31

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
545	gi7022824	Homo sapiens	cDNA FLJ10656 fis, clone NT2RP2006038.	1574	99
545	gi6841138	Homo sapiens	HSPC099 mRNA, partial cds.	248	36
545	AAG02788	Homo sapiens	Human secreted protein, SEQ ID NO: 6869.	234	85
546	AAB71914	Homo sapiens	Human ISOM-6.	1142	98
546	gi3876969	Caenorhabditis elegans	Similarity to Brugia peptidylprolyl isomerase (TR:G984562), contains similarity to Pfam domain: PF00076 (RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)), Score=62.0, E-value=4.2e-15, N=1; PF00160 (Cyclophilin type peptidyl-prolyl cis-trans isomerase), Score=78.1, E-value=3.7e-22, N=1	658	52
546	AAG02246	Homo sapiens	Human secreted protein, SEQ ID NO: 6327.	573	100
547	gi603635	Saccharomyces cerevisiae	Yel044wp	133	25
548	gi5262665	Homo sapiens	mRNA; cDNA DKFZp564B0769 (from clone DKFZp564B0769); partial cds.	1455	99
548	gi6841172	Homo sapiens	HSPC261	716	99
548	gi12803875	Homo sapiens	, Similar to splicing factor, arginine/serine-rich 4, clone MGC:3920, mRNA, complete cds.	352	33
549	gi7582298	Homo sapiens	BM-013	704	100
549	gi9558483	Ciona savignyi	PEM-3	434	55
549	gi1644450	Caenorhabditis elegans	MEX-3	362	65
550	gi4883433	Homo sapiens	mRNA for membrane transport protein (XK gene).	2148	100
550	gi6502963	Mus musculus	KX antigen	1797	81
550	gi2580580	Homo sapiens	testis-specific XK Related Y (XKRY) mRNA, complete cds.	157	31
551	gi7670746	Homo sapiens	UDP-glucose:glycoprotein glucosyltransferase 1 precursor, mRNA, complete cds.	8075	99
551	gi13275621	synthetic construct	Rat RUGT	7371	91
551	gi7677176	Rattus norvegicus	UDP-glucose glycoprotein:glucosyltransferase precursor	7371	91
552	gi7688985	Homo sapiens	uncharacterized bone marrow protein BM045	390	72
553	gi12655091	Homo sapiens	, AD-003 protein, clone MGC:783, mRNA, complete cds.	1177	100
553	gi6523799	Homo sapiens	adrenal gland protein AD-003 mRNA, complete cds.	1168	99
553	gi7105659	Caenorhabditis elegans	contains similarity to Streptomyces peucetius carminomycin 4-O-methyltransferase (GB:L13453)	425	39
554	gi7582282	Homo sapiens	BM-005	3445	99
554	gi7022933	Homo sapiens	cDNA FLJ10725 fis, clone NT2RP3001214.	3312	100
554	gi10435575	Homo sapiens	cDNA FLJ13534 fis, clone PLACE1006445.	1648	100
555	gi12751374	Homo sapiens	paraoxanase-3 mRNA, partial cds.	1819	99
555	gi1333634	Homo sapiens	paraoxanase 3 (PON3) mRNA, 3' end of cds.	1741	98
555	gi12743899	Oryctolagus	paraoxanase 3	1542	82

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
		cuniculus			
556	gi7022174	Homo sapiens	cDNA FLJ10252 fis, clone HEMBB1000807.	2826	100
556	gi11596985	Homo sapiens	chromosome 14 clone RP11-361H10 map 14q24.3, complete sequence.	559	36
556	gi7020945	Homo sapiens	cDNA FLJ20689 fis, clone KAlA2890.	510	39
557	gi10434683	Homo sapiens	cDNA FLJ12917 fis, clone NT2RP2004568, weakly similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.	2879	99
557	gi13384106	Homo sapiens	RNA helicase-like protein (RHLP) mRNA, complete cds.	2817	99
557	gi7020811	Homo sapiens	cDNA FLJ20596 fis, clone KAT08049.	2020	99
558	gi4760710	Brassica rapa	SLL2-S9-protein	284	43
558	gi1669601	Arabidopsis thaliana	AR401	280	44
558	gi557805	Saccharomyces cerevisiae	orf, len: 257, CAI: 0.13	327	34
559	gi13548677	Homo sapiens	MKP-7 mRNA for MAPK phosphatase-7, complete cds.	3418	100
559	gi13990989	Mus musculus	MAP kinase phosphatase-7	3093	90
559	AAB20325	Homo sapiens	Human protein phosphatase and kinase protein-4.	3021	90
560	gi10433965	Homo sapiens	cDNA FLJ12464 fis, clone NT2RM1000780.	2196	97
560	gi10434795	Homo sapiens	cDNA FLJ12992 fis, clone NT2RP3000149.	2196	97
560	gi10438048	Homo sapiens	cDNA: FLJ21857 fis, clone HEP02294.	2151	94
561	gi10438048	Homo sapiens	cDNA: FLJ21857 fis, clone HEP02294.	2276	97
561	gi10433965	Homo sapiens	cDNA FLJ12464 fis, clone NT2RM1000780.	2159	94
561	gi10434795	Homo sapiens	cDNA FLJ12992 fis, clone NT2RP3000149.	2159	94
562	gi10433965	Homo sapiens	cDNA FLJ12464 fis, clone NT2RM1000780.	2443	99
562	gi10434795	Homo sapiens	cDNA FLJ12992 fis, clone NT2RP3000149.	2443	99
562	gi10438048	Homo sapiens	cDNA: FLJ21857 fis, clone HEP02294.	2398	96
563	gi11137965	Homo sapiens	tRNA isopentenylpyrophosphate transferase precursor RNA, complete cds.	2158	100
563	gi7019915	Homo sapiens	cDNA FLJ20061 fis, clone COL01383.	1719	100
563	gi9803035	Caenorhabditis elegans	contains similarity to Pfam domain PF00096 (zf-C2H2), Score=12.0, E-value=1.1, N=1	407	32
564	gi7023103	Homo sapiens	cDNA FLJ10826 fis, clone NT2RP4001100.	2171	100
564	gi10434339	Homo sapiens	cDNA FLJ12690 fis, clone NT2RM4002567.	2171	100
564	gi10433458	Homo sapiens	cDNA FLJ12068 fis, clone HEMBB1002329.	2166	99
565	gi7019829	Homo sapiens	cDNA FLJ20011 fis, clone ADKA03432.	865	100
565	gi10438448	Homo sapiens	cDNA: FLJ22168 fis, clone HRC00618.	865	100
565	AAG02581	Homo sapiens	Human secreted protein, SEQ ID NO: 6662.	445	98
566	gi11558482	Homo sapiens	mRNA for B-cell lymphoma/leukaemia 11A extra long form (BCL11A-XL gene).	1543	99
566	gi12150278	Homo sapiens	C2H2-type zinc-finger protein mRNA, complete cds.	1039	99
566	gi6652688	Mus musculus	C2H2-type zinc finger protein	1033	98

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
567	gi12053249	Homo sapiens	mRNA; cDNA DKFZp434A155 (from clone DKFZp434A155); complete cds.	994	100
567	AAAY73435	Homo sapiens	Human secreted protein clone yd73_1 protein sequence SEQ ID NO:92.	994	100
567	AAB43698	Homo sapiens	Human cancer associated protein sequence SEQ ID NO:1143.	752	95
568	gi12053249	Homo sapiens	mRNA; cDNA DKFZp434A155 (from clone DKFZp434A155); complete cds.	752	95
568	AAAY73435	Homo sapiens	Human secreted protein clone yd73_1 protein sequence SEQ ID NO:92.	752	95
568	AAB43698	Homo sapiens	Human cancer associated protein sequence SEQ ID NO:1143.	853	100
569	gi8096260	Homo sapiens	gene for Nop10p, complete cds.	344	100
569	gi8096476	Homo sapiens	mRNA for Nop10p, complete cds.	344	100
569	gi14424489	Homo sapiens	, nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs), clone MGC:19486, mRNA, complete cds.	344	100
570	gi11595476	Homo sapiens	mRNA for RPB11b1beta protein (POLR2J2 gene).	633	100
570	AAB58870	Homo sapiens	Breast and ovarian cancer associated antigen protein sequence SEQ ID 578.	409	100
570	gi11595474	Homo sapiens	mRNA for RPB11b1alpha protein (POLR2J2 gene).	247	97
571	gi7239381	Homo sapiens	guanine nucleotide exchange factor smgGDS (RAP1GDS1) mRNA, alternatively spliced, complete cds.	2995	99
571	gi13111713	Homo sapiens	, RAP1, GTP-GDP dissociation stimulator 1, clone MGC:2897, mRNA, complete cds.	2994	99
571	gi6942013	Homo sapiens	exchange factor smgGDS mRNA, complete cds, alternatively spliced.	2991	99
572	gi12002978	Homo sapiens	mitosin-associated protein MITAP1 (MITAP1) mRNA, complete cds.	1736	100
572	gi12043569	Homo sapiens	Nudel mRNA, complete cds.	1736	100
572	gi13775593	Homo sapiens	endooligopeptidase A mRNA, complete cds.	1720	99
573	gi7022325	Homo sapiens	cDNA FLJ10350 fis, clone NT2RM2001131.	1243	100
573	gi12052730	Homo sapiens	mRNA; cDNA DKFZp761F19121 (from clone DKFZp761F19121).	1243	100
573	gi3417386	Mus musculus	microtubule-associated protein, MAP-115	428	48
574	gi7022502	Homo sapiens	cDNA FLJ10458 fis, clone NT2RP1001457, highly similar to Homo sapiens partial mRNA for beta-transducin family protein.	2555	100
574	gi3687833	Xenopus laevis	notchless	2149	82
574	gi12643028	Oryza sativa	Putative Notchless protein homolog	1110	52
575	AAAY51115	Homo sapiens	Human HSEC6 protein.	3767	99
575	gi1163174	Rattus norvegicus	similar to yeast Sec6p, Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author	3606	94
575	AAB49655	Homo sapiens	Human SEC7 protein sequence SEQ ID 14.	2737	89
576	gi7020303	Homo sapiens	cDNA FLJ20300 fis, clone HEP06465.	1697	99
576	AAB67575	Homo sapiens	Amino acid sequence of a human hydrolytic enzyme HYENZ7.	759	47

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
576	gi10434892	Homo sapiens	cDNA FLJ13055 fis, clone NT2RP3001538, weakly similar to HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.	755	47
577	AAR15222	Homo sapiens	Chronic myelogenous leukaemia-derived myeloid-related protein.	513	100
577	gi32402	Homo sapiens	Human mRNA for HP-1, a member of the corticostatin/defensin family.	493	100
577	gi181527	Homo sapiens	Human neutrophil peptide (defensin) 1 mRNA, complete cds.	493	100
578	AAV41716	Homo sapiens	Human PRO860 protein sequence.	5224	100
578	AAB44272	Homo sapiens	Human PRO860 (UNQ421) protein sequence SEQ ID NO:211.	5224	100
578	gi14042832	Homo sapiens	cDNA FLJ14946 fis, clone PLACE2000034, weakly similar to LAR PROTEIN PRECURSOR (EC 3.1.3.48).	3746	93
579	gi7021880	Homo sapiens	cDNA FLJ10054 fis, clone HEMBA1001310.	2306	100
579	gi12653981	Homo sapiens	, TRIAD3 protein, clone MGC:998, mRNA, complete cds.	2306	100
579	gi7109299	Homo sapiens	TRIAD3 mRNA, partial cds.	2013	100
580	gi3288457	Homo sapiens	mRNA for C2 domain containing PI3-kinase.	7615	99
580	gi3059227	Rattus norvegicus	phosphoinositide 3-kinase	3988	80
580	gi3041786	Mus musculus	Phosphoinositide 3-Kinase-C2gamma	3984	78
581	gi10437125	Homo sapiens	cDNA: FLJ21103 fis, clone CAS04883.	1802	99
581	gi7020867	Homo sapiens	cDNA FLJ20635 fis, clone KAT03466.	786	52
582	gi13937952	Homo sapiens	, Similar to upregulated during skeletal muscle growth 5, clone MGC:14697, mRNA, complete cds.	297	100
582	gi6851054	Rattus norvegicus	DAPIT protein	278	91
582	gi9843791	Mus musculus	stretch regulated skeletal muscle protein	259	84
583	gi7582286	Homo sapiens	BM-007	599	100
583	AAG02907	Homo sapiens	Human secreted protein, SEQ ID NO: 6988.	477	98
583	gi3878572	Caenorhabditis elegans	M01F1.6	161	28
584	gi13477103	Homo sapiens	, clone MGC:1012, mRNA, complete cds.	3001	99
584	gi12052999	Homo sapiens	mRNA; cDNA DKFZp434E1711 (from clone DKFZp434E1711); complete cds.	2619	98
584	gi7020996	Homo sapiens	cDNA FLJ20721 fis, clone HEP15722.	2402	100
585	AAW48892	Homo sapiens	Human guanylate binding protein B (HGBPB).	2645	94
585	gi12803663	Homo sapiens	, guanylate binding protein 1, interferon-inducible, 67kD, clone MGC:3949, mRNA, complete cds.	2000	66
585	gi183002	Homo sapiens	Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.	2000	66
586	gi7023366	Homo sapiens	cDNA FLJ10983 fis, clone PLACE1001781, weakly similar to PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8).	3218	99
586	gi12052930	Homo sapiens	mRNA; cDNA DKFZp566B1524 (from clone DKFZp566B1524); complete cds.	3216	99
586	gi3395586	Schizosaccharomyces pombe	similarity to phosphomannomutases	1211	43

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
587	gi13537208	Mus musculus	Mel18 and Bmi1 like ring finger	347	40
587	gi2440074	Homo sapiens	mRNA for RNF3A (DONG1) ring finger protein.	347	37
587	gi13537206	Homo sapiens	hMBLR mRNA, complete cds.	345	40
588	gi14042249	Homo sapiens	cDNA FLJ14610 fis, clone NT2RP1000958, weakly similar to AUTOANTIGEN NGP-1.	2797	99
588	gi14042246	Homo sapiens	cDNA FLJ14608 fis, clone NT2RP1000915, weakly similar to AUTOANTIGEN NGP-1.	2741	99
588	gi6457340	Homo sapiens	E2IG3 (E2IG3) mRNA, complete cds.	2650	100
589	gi7020925	Homo sapiens	cDNA FLJ20673 fis, clone KAIA4464.	2232	100
589	gi7682684	Homo sapiens	phosphoprotein associated with GEMs (PAG) mRNA, complete cds.	2222	99
589	gi7707799	Rattus norvegicus	Csk binding protein Cbp	1696	78
590	gi6682873	Homo sapiens	rec mRNA, complete cds.	2002	100
590	gi7230612	Rattus norvegicus	small rec	1916	95
590	gi3881771	Caenorhabditis elegans	contains similarity to Pfam domain: PF01529 (DHHC zinc finger domain), Score=137.4, E-value=8.4e-38, N=1	586	39
591	gi439522	Mus musculus	ribosomal protein S3	678	100
591	gi57728	Rattus rattus	ribosomal protein S3 (AA 1-243)	678	100
591	gi13111933	Homo sapiens	, ribosomal protein S3, clone MGC:3657, mRNA, complete cds.	678	100
592	gi6599070	Homo sapiens	mRNA for LIM domains containing protein 1.	3675	99
592	gi6599307	Mus musculus	LIM domains containing protein 1	2728	76
592	gi13548632	Homo sapiens	partial LIMD1 gene for LIM domains containing 1, exons 1-2, complete sequence.	2690	99
593	gi7020974	Homo sapiens	cDNA FLJ20706 fis, clone KAIA1273.	2824	98
593	gi12082725	Mus musculus	B cell phosphoinositide 3-kinase adaptor	411	29
593	AAG02945	Homo sapiens	Human secreted protein, SEQ ID NO: 7026.	526	100
594	gi11596144	Homo sapiens	STE20-like kinase mRNA, partial cds.	5159	99
594	gi3452473	Rattus norvegicus	serine/threonine protein kinase TAO1	5117	98
594	AAV55937	Homo sapiens	Human SULU3 protein.	4045	100
595	gi695802	Homo sapiens	transcription factor SL1 mRNA, partial cds.	1693	99
595	gi1842206	Mus musculus	TAFI68	1326	76
596	gi7020363	Homo sapiens	cDNA FLJ20335 fis, clone HEP11429.	2940	99
596	AAB65680	Homo sapiens	Novel protein kinase, SEQ ID NO: 208.	2940	99
596	AAB32078	Homo sapiens	Human secreted protein BLAST search protein SEQ ID NO: 136.	826	100
597	gi7020747	Homo sapiens	cDNA FLJ20558 fis, clone KAT11870.	2990	100
597	gi12053175	Homo sapiens	mRNA; cDNA DKFZp434A172 (from clone DKFZp434A172); complete cds.	2990	100
597	gi10439123	Homo sapiens	cDNA: FLJ22650 fis, clone HSI07344.	2166	100
598	gi7023601	Homo sapiens	cDNA FLJ11127 fis, clone PLACE1006225.	1897	100
598	gi12224968	Homo sapiens	mRNA; cDNA DKFZp667E105 (from clone DKFZp667E105).	620	100
598	gi14043433	Homo sapiens	, clone IMAGE:3952677, mRNA, partial cds.	549	41
599	gi6483296	Homo sapiens	CDH9 mRNA for cadherin-9, complete cds.	4132	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
599	gi867999	Gallus gallus	chicken cadherin-6B	3044	72
599	gi974185	Homo sapiens	mRNA for cadherin-6, complete cds.	3032	72
600	gi5734605	Homo sapiens	mRNA for KARP-1-binding protein 3, complete cds.	750	51
600	gi5734601	Homo sapiens	mRNA for KARP-1-binding protein 1 (KAB1), complete cds.	750	51
600	gi5734603	Homo sapiens	mRNA for KARP-1-binding protein 2 (KAB2), complete cds.	750	51
601	gi10434848	Homo sapiens	cDNA FLJ13028 fis, clone NT2RP3001055, weakly similar to Drosophila melanogaster separation anxiety protein (san) mRNA.	889	100
601	gi10435107	Homo sapiens	cDNA FLJ13194 fis, clone NT2RP3004378, weakly similar to Drosophila melanogaster separation anxiety protein (san) mRNA.	889	100
601	AAB56739	Homo sapiens	Human prostate cancer antigen protein sequence SEQ ID NO:1317.	874	98
602	gi13325182	Homo sapiens	, clone IMAGE:3638994, mRNA, partial cds.	897	100
602	gi12654203	Homo sapiens	, clone IMAGE:3449323, mRNA, partial cds.	560	100
602	gi4514314	Bacillus halodurans	YlqF	260	39
603	gi10954046	Homo sapiens	oxidation protection protein (OXR1) mRNA, complete cds.	1034	97
603	gi13540300	Mus musculus	nucleolar protein C7B	1431	94
603	gi7021988	Homo sapiens	cDNA FLJ10125 fis, clone HEMBA1002954.	1441	99
604	gi1150495	Mus musculus	homology to nucleosome assembly proteins; specifically expressed in neurons	211	36
604	gi1161252	Glycine max	nucleosome assembly protein 1	136	40
604	gi5931610	Homo sapiens	mRNA for Nucleosome Assembly Protein 1-like 2, complete cds.	196	37
605	gi7547029	Homo sapiens	GAP-like protein (N61) mRNA, complete cds.	4684	99
605	gi7688683	Homo sapiens	kinesin heavy chain-like protein (KHCHP) mRNA, complete cds.	822	100
605	AAG03378	Homo sapiens	Human secreted protein, SEQ ID NO: 7459.	633	99
606	gi7022593	Homo sapiens	cDNA FLJ10511 fis, clone NT2RP2000656.	1425	100
606	gi12224996	Homo sapiens	mRNA; cDNA DKFZp667G248 (from clone DKFZp667G248).	1031	100
606	gi10436327	Homo sapiens	cDNA FLJ13991 fis, clone Y79AA1002115.	803	100
607	gi8885998	Rattus norvegicus	neuronal C-SRC tyrosine-specific protein kinase	2826	98
607	gi201057	Mus musculus	tyrosine-specific protein kinase	2822	98
607	gi338460	Homo sapiens	Human c-src-1 proto-oncogene, exon 12.	2815	98
608	gi7243633	Homo sapiens	RB-associated KRAB repressor (RBAK) mRNA, complete cds.	3993	100
608	gi7243635	Mus musculus	RB-associated KRAB repressor	3025	78
608	gi10434235	Homo sapiens	cDNA FLJ12629 fis, clone NT2RM4001828, moderately similar to ZINC FINGER PROTEIN 84.	1881	73
609	gi7008402	Homo sapiens	kappa B-ras 1 mRNA, complete cds.	982	100
609	gi14042659	Homo sapiens	cDNA FLJ14843 fis, clone	978	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			PLACE1000040, weakly similar to TRANSFORMING PROTEIN P21/K-RAS 2B.		
609	gi7239257	Mus musculus	kappaB-Ras1	952	94
610	gi13625164	Homo sapiens	ankyrin mRNA, complete cds.	426	100
610	gi12698638	Homo sapiens	ankyrin-repeat family A protein 2 (ANKRA2) mRNA, complete cds.	426	100
610	gi10434525	Homo sapiens	cDNA FLJ12814 fis, clone NT2RP2002520, weakly similar to Homo sapiens transcription factor RFX-B (RFXB) mRNA.	426	100
611	gi7959841	Homo sapiens	PRO1853	510	100
611	AAG01282	Homo sapiens	Human secreted protein, SEQ ID NO: 5363.	301	100
612	gi5757703	Mus musculus	syntrophin-associated serine-threonine protein kinase	7464	92
612	gi13537204	Homo sapiens	mRNA for MAST205, complete cds.	4616	68
612	gi406058	Mus musculus	protein kinase	4569	65
613	gi7020724	Homo sapiens	cDNA FLJ20545 fis, clone KAT11476.	1780	100
613	AAB63186	Homo sapiens	Human secreted protein sequence encoded by gene 3 SEQ ID NO:112.	1693	100
613	gi7243701	Drosophila melanogaster	WDS	1574	91
614	gi13383476	Homo sapiens	NUB1 (NUB1) mRNA, complete cds.	3109	100
614	gi5360093	Homo sapiens	NY-REN-18 antigen mRNA, complete cds.	2958	95
614	gi863014	Mus musculus	BS4 peptide	2671	84
615	AAB87345	Homo sapiens	Human gene 4 encoded secreted protein HDPFY41, SEQ ID NO:86.	4534	100
615	gi4886489	Homo sapiens	mRNA; cDNA DKFZp564L2123 (from clone DKFZp564L2123); partial cds.	2892	99
615	gi12711793	Homo sapiens	estrogen regulated LIV-1 protein (LIV-1) mRNA, complete cds.	1171	39
616	gi7638247	Homo sapiens	mesenchymal stem cell protein DSCD75 mRNA, complete cds.	1063	100
616	gi12654929	Homo sapiens	, mesenchymal stem cell protein DSCD75, clone MGC:5515, mRNA, complete cds.	1063	100
616	AAB03956	Homo sapiens	Human mesenchymal stem cell polypeptide.	1063	100
617	gi7582304	Homo sapiens	BM-016	584	100
617	AAW78199	Homo sapiens	Human secreted protein encoded by gene 74 clone HGBAC11.	562	98
617	AAW85610	Homo sapiens	Secreted protein clone eh80 1.	562	98
618	gi13603398	Homo sapiens	mRNA for SEZ6L, complete cds.	4199	98
618	gi13185723	Homo sapiens	n 1755 can be A, G, C, or T	2164	49
618	AAB70537	Homo sapiens	Human PRO7 protein sequence SEQ ID NO:14.	2164	49
619	gi3880445	Caenorhabditis elegans	contains similarity to Pfam domain: PF02214 (K+ channel tetramerisation domain), Score=79.5, E-value=2.3e-20, N=1	327	40
619	AAV34129	Homo sapiens	Human potassium channel K+Hnov28.	195	40
619	AAZ11907_aal	Homo sapiens	Human potassium channel K+Hnov28 cDNA (5' splice variant 1).	195	40
620	gi10437116	Homo sapiens	cDNA: FLJ21097 fis, clone CAS03931.	1146	100
620	gi14250732	Homo sapiens	, chromosome 11 open reading frame 14, clone MGC:12847, mRNA, complete cds.	1146	100
620	gi13276621	Homo sapiens	mRNA; cDNA DKFZp761G1913 (from	378	43

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			clone DKFZp761G1913).		
621	gi10437078	Homo sapiens	cDNA: FLJ21069 fis, clone CAS01594.	955	58
621	gi5911935	Homo sapiens	mRNA; cDNA DKFZp586N1922 (from clone DKFZp586N1922); partial cds.	867	100
621	AAB27870	Homo sapiens	Protein fragment encoded by gene 27.	657	100
622	gi13097159	Homo sapiens	, tumor protein, translationally-controlled 1, clone MGC:5308, mRNA, complete cds.	898	100
622	gi14043771	Homo sapiens	, clone MGC:14243, mRNA, complete cds.	898	100
622	gi7573519	Homo sapiens	TPT1 gene for translationally controlled tumor protein (TCTP), exons 1-6.	898	100
623	gi7020339	Homo sapiens	cDNA FLJ20320 fis, clone HEP08923.	1135	100
623	AAB18972	Homo sapiens	Amino acid sequence of a human transmembrane protein.	1135	100
623	gi1314162	Schizosaccharomyces pombe	seven transmembrane protein	217	29
624	gi6467990	Mus musculus	PDZ domain actin binding protein Shroom	4816	66
624	gi6467992	Mus musculus	actin binding protein ShroomS	4816	66
624	gi13938323	Homo sapiens	, Similar to shroom, clone IMAGE:3349317, mRNA, partial cds.	4006	99
625	gi12804029	Homo sapiens	, clone IMAGE:3940519, mRNA, partial cds.	1551	100
625	AAAY21850	Homo sapiens	Human signal peptide-containing protein (SIGP) (clone ID 1880830).	1109	100
625	gi8655657	Homo sapiens	mRNA; cDNA DKFZp762O076 (from clone DKFZp762O076).	593	57
626	gi7328140	Homo sapiens	mRNA; cDNA DKFZp762D096 (from clone DKFZp762D096); partial cds.	601	100
626	gi13436341	Homo sapiens	, Similar to RIKEN cDNA 1600014C10 gene, clone MGC:10922, mRNA, complete cds.	384	100
627	gi1293559	Mus musculus	astrotactin	4312	95
627	gi6502571	Mus musculus	astrotactin2	2580	51
627	gi6502573	Homo sapiens	astrotactin2 (ASTN2) mRNA, complete cds.	2569	51
628	AAAY73387	Homo sapiens	HTRM clone 3340290 protein sequence.	1439	95
628	AAAY48312	Homo sapiens	Human prostate cancer-associated protein 9.	1073	84
628	gi12654077	Homo sapiens	, clone IMAGE:3458173, mRNA, partial cds.	1045	86
629	gi11095188	Homo sapiens	dipeptidyl peptidase 8 (DPP8) mRNA, complete cds.	3521	99
629	gi14042790	Homo sapiens	cDNA FLJ14920 fis, clone PLACE1007416, weakly similar to DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5).	2457	99
629	gi7020273	Homo sapiens	cDNA FLJ20283 fis, clone HEP04088.	2483	100
630	gi11095188	Homo sapiens	dipeptidyl peptidase 8 (DPP8) mRNA, complete cds.	2560	99
630	gi14042790	Homo sapiens	cDNA FLJ14920 fis, clone PLACE1007416, weakly similar to DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5).	2457	99
630	gi11095192	Homo sapiens	dipeptidyl peptidase 8 (DPP8) mRNA, partial cds, alternatively spliced.	2482	100
631	gi7020611	Homo sapiens	cDNA FLJ20481 fis, clone KAT07534.	2211	99
631	AAAY57908	Homo sapiens	Human transmembrane protein HTMPN-	975	44

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			32.		
631	AAB54284	Homo sapiens	Human pancreatic cancer antigen protein sequence SEQ ID NO:736.	516	40
632	gi35700	Homo sapiens	Human mRNA for phosphoribosyl pyrophosphate synthetase subunit II (EC 2.7.6.1).	1596	99
632	gi206434	Rattus norvegicus	phosphoribosyl pyrophosphate synthetase II	1585	98
632	gi56979	Rattus norvegicus	ribose-phosphate pyrophosphokinase subunit II (AA 1-318)	1585	98
633	gi11181620	Homo sapiens	Rag D mRNA, complete cds.	1276	100
633	gi6808148	Homo sapiens	mRNA; cDNA DKFZp761H171 (from clone DKFZp761H171); partial cds.	1276	100
633	AAB56443	Homo sapiens	Human prostate cancer antigen protein sequence SEQ ID NO:1021.	1276	100
634	gi6807893	Homo sapiens	mRNA; cDNA DKFZp434H2226 (from clone DKFZp434H2226); partial cds.	1079	100
635	gi10435042	Homo sapiens	cDNA FLJ13152 fis, clone NT2RP3003385, highly similar to Mus musculus SKD3 mRNA.	3495	100
635	gi4958935	Rattus norvegicus	suppressor of potassium transport defect 3	3085	88
635	gi563129	Mus musculus	SKD3	3066	88
636	AAB20322	Homo sapiens	Human protein phosphatase and kinase protein-1.	1770	100
636	gi1903458	Dictyostelium discoideum	myosin heavy chain kinase B	236	32
636	gi2104701	Mus musculus	elongation factor-2 kinase	199	29
637	gi7670003	Homo sapiens	mRNA; cDNA DKFZp434P0531 (from clone DKFZp434P0531).	1850	100
637	gi7417474	Homo sapiens	chromosome 14 clone RP11-493G17 and CTD-2516D11 map 14q24.3, complete sequence.	1251	49
637	gi7018538	Homo sapiens	mRNA; cDNA DKFZp434P0111 (from clone DKFZp434P0111); partial cds.	330	43
638	gi7022367	Homo sapiens	cDNA FLJ10375 fis, clone NT2RM2001950.	3056	100
638	AAV53026	Homo sapiens	Human secreted protein clone cn922_5 protein sequence SEQ ID NO:58.	1752	95
638	gi4336692	Drosophila melanogaster	Abnormal X segregation	816	37
639	gi7020972	Homo sapiens	cDNA FLJ20705 fis, clone KA1A1571.	3641	99
639	gi12007334	Homo sapiens	IRS-1 PH domain binding protein PHIP mRNA, complete cds.	3632	99
639	gi14286226	Homo sapiens	, pleckstrin homology domain interacting protein, clone MGC:15187, mRNA, complete cds.	3632	99
640	gi7689025	Homo sapiens	uncharacterized hypothalamus protein HT013 mRNA, complete cds.	978	96
641	gi9937505	Homo sapiens	PLIC-2 mRNA, complete cds.	3167	100
641	gi6563288	Homo sapiens	ubiquitin-like product Chap1/Dsk2 mRNA, complete cds.	3162	99
641	AAB47122	Homo sapiens	Human Chap1.	3162	99
642	AAV53001	Homo sapiens	Human secreted protein clone dn834_1 protein sequence SEQ ID NO:8.	811	100
642	AAG01114	Homo sapiens	Human secreted protein, SEQ ID NO: 5195.	641	99
642	gi12652989	Homo sapiens	, clone MGC:2495, mRNA, complete cds.	489	57
643	gi7021064	Homo sapiens	cDNA FLJ20761 fis, clone HEP00317.	2240	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
643	gi10438264	Homo sapiens	cDNA: FLJ22019 fis, clone HEP07982.	2187	98
643	gi577428	Rattus norvegicus	Ca ²⁺ -dependent activator protein; calcium-dependent actin-binding protein	1787	77
644	gi7023651	Homo sapiens	cDNA FLJ11159 fis, clone PLACE1006966.	2865	99
644	gi7023118	Homo sapiens	cDNA FLJ10835 fis, clone NT2RP4001210.	1253	100
644	gi600058	Saccharomyces cerevisiae	N1342	710	39
645	gi7020012	Homo sapiens	cDNA FLJ20121 fis, clone COL05942.	1334	99
646	gi14336697	Homo sapiens	16p13.3 sequence section 2 of 8.	609	100
646	gi13436122	Homo sapiens	, non-metastatic cells 4, protein expressed in, clone MGC:11088, mRNA, complete cds.	609	100
646	gi1945762	Homo sapiens	H.sapiens mRNA for nucleoside-diphosphate kinase.	609	100
647	AAB24225	Homo sapiens	Human vesicle associated protein 4 SEQ ID NO:4.	2946	99
647	gi10439139	Homo sapiens	cDNA: FLJ22662 fis, clone HSI08080.	2703	99
647	AAB58427	Homo sapiens	Lung cancer associated polypeptide sequence SEQ ID 765.	1711	99
648	gi7020604	Homo sapiens	cDNA FLJ20477 fis, clone KAT07271.	2639	99
648	gi6672090	Drosophila melanogaster	Vegetable	578	32
649	gi12802986	Homo sapiens	, ring finger protein 24, clone MGC:1815, mRNA, complete cds.	811	100
649	gi5420200	Homo sapiens	Novel human mRNA from chromosome 20, similar to SW:GOLI_DROME Q06003 GOLIATH PROTEIN.	811	100
649	gi5102892	Homo sapiens	mRNA full length insert cDNA clone EUROIMAGE 566628.	566	100
650	gi6841346	Homo sapiens	HSPC054	497	98
651	gi7209305	Homo sapiens	mRNA for FLJ00002 protein, partial cds.	7637	100
651	gi6599226	Homo sapiens	mRNA; cDNA DKFZp434L0827 (from clone DKFZp434L0827); partial cds.	3519	100
651	gi10440406	Homo sapiens	mRNA for FLJ00036 protein, partial cds.	3457	99
652	gi7018505	Homo sapiens	mRNA; cDNA DKFZp434E2220 (from clone DKFZp434E2220).	2470	100
652	gi14042579	Homo sapiens	cDNA FLJ14796 fis, clone NT2RP4001235.	2466	99
652	gi7018507	Homo sapiens	mRNA; cDNA DKFZp434O0420 (from clone DKFZp434O0420).	2466	99
653	gi552196	Plasmodium lophurae	histidine-rich protein	192	40
653	gi160362	Plasmodium falciparum	knob protein	178	42
653	gi3845095	Plasmodium falciparum	knob-associated His-rich protein	172	40
654	AAAY70539	Homo sapiens	Human Factor 8 Homologue.	1353	83
654	gi14043498	Homo sapiens	, Similar to neuropilin 1, clone MGC:12920, mRNA, complete cds.	189	34
654	gi7271465	Homo sapiens	soluble neuropilin-1 mRNA, complete cds.	189	34
655	gi7019959	Homo sapiens	cDNA FLJ20087 fis, clone COL03793.	3964	100
655	gi13569705	Homo sapiens	channel kinase 2 (CHAK2) mRNA, complete cds.	3942	99
655	AAAY95433	Homo sapiens	Human calcium channel SOC-2/CRAC-1 C-terminal polypeptide.	1172	71
656	gi6094668	Homo sapiens	BAC clone RP11-343N14 from 2,	208	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			complete sequence.		
656	gi10435833	Homo sapiens	cDNA FLJ13729 fis, clone PLACE3000121, weakly similar to VESICULAR TRAFFIC CONTROL PROTEIN SEC15.	208	100
656	gi2827162	Rattus norvegicus	rsec15	160	73
657	gi10434153	Homo sapiens	cDNA FLJ12580 fis, clone NT2RM4001116, weakly similar to HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.	1806	99
657	gi12053255	Homo sapiens	mRNA; cDNA DKFZp434D105 (from clone DKFZp434D105); complete cds.	1806	99
657	gi5901808	Drosophila melanogaster	BcDNA.GH03694	619	56
658	gi1181618	Homo sapiens	Rag C mRNA, complete cds.	2072	100
658	gi12007486	Homo sapiens	GTPase-interacting protein 2 mRNA, complete cds.	2069	99
658	gi13529335	Mus musculus	Similar to Rag C protein	2039	98
659	gi13537208	Mus musculus	Mel18 and Bmi1 like ring finger	347	40
659	gi2440074	Homo sapiens	mRNA for RNF3A (DONG1) ring finger protein.	347	37
659	gi13537206	Homo sapiens	hMBLR mRNA, complete cds.	345	40
660	gi7023690	Homo sapiens	cDNA FLJ11184 fis, clone PLACE1007507.	1043	99
661	gi7020878	Homo sapiens	cDNA FLJ20641 fis, clone KAT02782.	2552	99
661	gi11992034	Rattus norvegicus	antisense RNA overlapping MCH protein	1609	65
662	AAB56646	Homo sapiens	Human prostate cancer antigen protein sequence SEQ ID NO:1224.	915	98
662	gi12053357	Homo sapiens	mRNA; cDNA DKFZp586G2122 (from clone DKFZp586G2122); complete cds.	900	100
662	AAB36598	Homo sapiens	Human FLEXHT-20 protein sequence SEQ ID NO:20.	791	59
663	AAW93947	Homo sapiens	Human regulatory molecule HRM-3 protein.	1732	100
663	gi3288459	Homo sapiens	mRNA for transcription elongation factor TFIIS.h.	1673	100
663	gi3288547	Mus musculus	transcription elongation factor TFIIS.h	1543	90
664	gi14042893	Homo sapiens	cDNA FLJ14984 fis, clone Y79AA1000349, highly similar to M.musculus Spnr mRNA for RNA binding protein.	3478	100
664	gi13377630	Homo sapiens	spermatid perinuclear RNA-binding protein mRNA, complete cds.	3459	99
664	gi12053237	Homo sapiens	mRNA; cDNA DKFZp434N214 (from clone DKFZp434N214); complete cds.	3406	100
665	gi10436573	Homo sapiens	cDNA FLJ14183 fis, clone NT2RP2004920, weakly similar to TRANSCRIPTIONAL REGULATOR ATRX.	4423	99
665	gi10434345	Homo sapiens	cDNA FLJ12693 fis, clone NT2RP1000324.	4369	99
665	AAB27235	Homo sapiens	Human EXMAD-13 SEQ ID NO: 13.	3346	100
666	gi9858154	Homo sapiens	tubby super-family protein (TUSP) mRNA, complete cds, alternatively spliced.	3598	100
666	gi9502082	Homo sapiens	tubby super-family protein (TUSP) mRNA, complete cds.	3556	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
666	gi9502080	Mus musculus	tubby super-family protein	3505	98
667	gi7106796	Homo sapiens	HSPC203	554	100
667	gi9963859	Homo sapiens	PTD019 mRNA, complete cds.	554	100
667	AAV35987	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 236.	554	100
668	gi6996442	Homo sapiens	CTL1 gene.	3398	99
668	gi6996589	Rattus norvegicus	CTL1 protein	3291	96
668	gi6996587	Torpedo marmorata	CTL1 protein	2454	71
669	gi6808165	Homo sapiens	mRNA; cDNA DKFZp761A052 (from clone DKFZp761A052).	2265	100
669	gi10439058	Homo sapiens	cDNA: FLJ22607 fis, clone HSI04846.	1992	100
669	gi7673616	Mus musculus	DXImx46e protein	1958	98
670	gi6808252	Homo sapiens	mRNA; cDNA DKFZp434D1319 (from clone DKFZp434D1319); partial cds.	2336	100
670	gi170035	Glycine max	N-75	221	27
670	gi18576	Glycine max	pre-pro polypeptide (AA -25 to 284)	219	27
671	AAW93947	Homo sapiens	Human regulatory molecule HRM-3 protein.	1116	99
671	gi3288459	Homo sapiens	mRNA for transcription elongation factor TFIIS.h.	1057	99
671	gi3288547	Mus musculus	transcription elongation factor TFIIS.h	950	86
672	gi10434615	Homo sapiens	cDNA FLJ12875 fis, clone NT2RP2003777.	1818	99
672	gi8778741	Arabidopsis thaliana	T30E16.12	254	27
672	gi6520214	Arabidopsis thaliana	ZCF61	228	29
673	AAB88424	Homo sapiens	Human membrane or secretory protein clone PSEC0197.	3032	99
673	gi9294464	Arabidopsis thaliana	long-chain-fatty-acid-CoA ligase-like protein	581	37
673	gi699196	Mycobacterium leprae	4-coumarate-coA ligase	326	45
674	gi7022969	Homo sapiens	cDNA FLJ10747 fis, clone NT2RP3001799.	3378	99
674	AAV86211	Homo sapiens	Nuclear transport protein clone hfb066 protein sequence.	1432	87
674	gi10439560	Homo sapiens	cDNA: FLJ23007 fis, clone LNG00451.	703	100
675	gi7021968	Homo sapiens	cDNA FLJ10111 fis, clone HEMBA1002696.	2753	99
675	gi14017768	Mus musculus	FLJ10111	2214	92
675	gi10440211	Homo sapiens	cDNA: FLJ23501 fis, clone LNG02837.	2160	90
676	gi7021968	Homo sapiens	cDNA FLJ10111 fis, clone HEMBA1002696.	2728	98
676	gi14017768	Mus musculus	FLJ10111	2200	90
676	gi10440211	Homo sapiens	cDNA: FLJ23501 fis, clone LNG02837.	2237	92
677	gi7019869	Homo sapiens	cDNA FLJ20036 fis, clone COL00219.	2834	100
677	gi12723779	Lactococcus lactis subsp. lactis	UNKNOWN PROTEIN	306	35
677	gi8885520	Streptococcus gordonii	streptococcal hemagglutinin	297	29
678	gi10437508	Homo sapiens	cDNA: FLJ21415 fis, clone COL04030.	1129	100
679	gi3135314	Homo sapiens	chromosome 7q22 sequence, complete sequence.	1226	100
679	gi6752287	Homo sapiens	Novel human gene mapping to chromosome X.	390	43

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
679	AAB28327	Homo sapiens	Human secreted protein BLAST search protein SEQ ID NO: 111.	265	100
680	gi3135314	Homo sapiens	chromosome 7q22 sequence, complete sequence.	1199	95
680	gi6752287	Homo sapiens	Novel human gene mapping to chromosome X.	363	41
680	AAB28327	Homo sapiens	Human secreted protein BLAST search protein SEQ ID NO: 111.	265	100
681	gi10439089	Homo sapiens	cDNA: FLJ22626 fis, clone HSI06109.	2120	99
681	gi11044557	Homo sapiens	Human DNA sequence from clone RP11-42415 on chromosome 6 Contains a novel gene, STSs, GSSs and a CpG island, complete sequence.	1185	64
681	gi12654241	Homo sapiens	, Similar to splicing factor, arginine/serine-rich 4 (SRp75), clone MGC:5283, mRNA, complete cds.	949	98
682	gi14042277	Homo sapiens	cDNA FLJ14626 fis, clone NT2RP2000288.	3029	99
682	gi7022410	Homo sapiens	cDNA FLJ10402 fis, clone NT2RM4000457.	2279	100
682	gi6841196	Homo sapiens	HSPC273	1086	100
683	gi2815604	Homo sapiens	Opa-interacting protein OIP2 mRNA, partial cds.	1364	100
683	AAB63276	Homo sapiens	Human breast cancer associated antigen protein sequence SEQ ID NO:638.	839	96
683	AAB63406	Homo sapiens	Human breast cancer associated antigen protein sequence SEQ ID NO:768.	839	96
684	AAB07228	Homo sapiens	Human prostate cancer predisposing protein HPC2.	4325	100
684	AAAY99850	Homo sapiens	Human sulphatase G.	4315	99
684	gi10946497	Pan troglodytes	ELAC2	4283	98
685	gi7688979	Homo sapiens	uncharacterized bone marrow protein BM042	895	100
685	AAB36580	Homo sapiens	Human FLEXHT-2 protein sequence SEQ ID NO:2.	895	100
685	AAB34771	Homo sapiens	Human secreted protein fragment encoded by DNA clone vq23 1.	888	99
686	gi10438990	Homo sapiens	cDNA: FLJ22559 fis, clone HSI01591.	1897	100
686	gi8954034	Arabidopsis thaliana	F10K1.17	162	31
687	gi7020674	Homo sapiens	cDNA FLJ20515 fis, clone KAT09889.	2027	100
687	AAB20331	Homo sapiens	Human protein phosphatase and kinase protein-10.	1472	92
687	AAB73226	Homo sapiens	Human phosphatase NP 060746 h.	576	83
688	gi6688145	Homo sapiens	mRNA for NICE-3 protein, clone 1023j12.	1019	100
688	gi4689120	Homo sapiens	HSPC012	717	93
688	gi12655055	Homo sapiens	, DKFZP586G1722 protein, clone MGC:1147, mRNA, complete cds.	717	93
689	gi7023701	Homo sapiens	cDNA FLJ11190 fis, clone PLACE1007583.	1317	100
690	gi6469703	Mycobacterium tuberculosis	DipZ	203	31
691	gi13676779	Mus musculus	Arkadia	1939	93
691	gi13752369	Gallus gallus	ring finger protein	1888	91
691	gi13752371	Xenopus laevis	ring finger-H2 protein	1537	76
692	gi458255	Homo sapiens	Human X-linked PEST-containing	2849	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			transporter (XPCT) gene, exon 6.		
692	gi458247	Homo sapiens	Human X-linked PEST-containing transporter (XPCT) mRNA, partial cds.	2766	99
692	gi2944356	Mus musculus	X-linked PEST-containing transporter	2249	88
693	gi14042736	Homo sapiens	cDNA FLJ14888 fis, clone PLACE1003762.	2034	99
693	gi6841178	Homo sapiens	HSPC264	2019	99
694	gi7023413	Homo sapiens	cDNA FLJ11012 fis, clone PLACE1003190, weakly similar to SOF1 PROTEIN.	2377	99
694	gi14042745	Homo sapiens	cDNA FLJ14893 fis, clone PLACE1004302, weakly similar to SOF1 PROTEIN.	2377	99
694	gi5912184	Homo sapiens	mRNA; cDNA DKFZp564O0463 (from clone DKFZp564O0463); partial cds.	1159	99
695	gi7022931	Homo sapiens	cDNA FLJ10724 fis, clone NT2RP3001176.	2683	99
695	gi14198202	Mus musculus	Similar to melanoma antigen recognized by T cells 2	2126	82
695	gi4826524	Homo sapiens	Novel human gene mapping to chromosome 1.	982	92
696	gi7022990	Homo sapiens	cDNA FLJ10761 fis, clone NT2RP3004669, weakly similar to ETHANOLAMINE KINASE (EC 2.7.1.82).	2119	99
696	gi9998952	Homo sapiens	ethanolamine kinase (EK11) mRNA, complete cds.	930	56
696	gi532128	Drosophila melanogaster	ethanolamine kinase	525	45
697	gi186774	Homo sapiens	Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.	986	38
697	gi5441615	Canis familiaris	zinc finger protein	988	37
697	gi38032	Homo sapiens	Human ZNF43 mRNA.	947	36
698	gi13537202	Homo sapiens	PC-LKC mRNA for protocadherin LKC, complete cds.	2877	100
698	gi7020017	Homo sapiens	cDNA FLJ20124 fis, clone COL06056.	2862	99
698	AAV01410	Homo sapiens	Secreted protein encoded by gene 28 clone HE9ND43.	963	100
699	gi7688977	Homo sapiens	uncharacterized bone marrow protein BM041	888	100
699	AAV86515	Homo sapiens	Human gene 71-encoded protein fragment, SEQ ID NO:430.	888	100
699	gi7018421	Homo sapiens	mRNA; cDNA DKFZp564J157 (from clone DKFZp564J157).	880	99
700	gi7209307	Homo sapiens	mRNA for FLJ00003 protein, partial cds.	1102	100
700	gi14276857	Homo sapiens	PC2-glutamine-rich-associated protein (PCQAP) mRNA, complete cds.	429	93
700	gi14043091	Homo sapiens	, clone IMAGE:3350171, mRNA, partial cds.	429	93
701	gi7020678	Homo sapiens	cDNA FLJ20517 fis, clone KAT10235.	2821	99
701	gi10177966	Arabidopsis thaliana	uridine kinase-like protein	1068	44
701	gi496728	Saccharomyces cerevisiae	uridine kinase	775	37
702	gi7022789	Homo sapiens	cDNA FLJ10634 fis, clone NT2RP2005654, weakly similar to CYSTEINE STRING PROTEIN.	1512	100
702	AAB67446	Homo sapiens	Amino acid sequence of a human	1512	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			chaperone polypeptide.		
702	AAG01952	Homo sapiens	Human secreted protein, SEQ ID NO: 6033.	422	98
703	gi7021321	Homo sapiens	Gemin4 mRNA, complete cds.	5481	99
703	gi10945430	Homo sapiens	chromosome 17 clone PAC P579 HC90, HC71AC, HC6 and HC56 genes, complete sequence.	5452	100
703	gi7018412	Homo sapiens	mRNA; cDNA DKFZp434D174 (from clone DKFZp434D174).	4359	99
704	gi9964287	Homo sapiens	hypertension-related calcium-regulated gene mRNA, complete cds.	1129	100
704	gi10434820	Homo sapiens	cDNA FLJ13008 fis, clone NT2RP3000456.	1129	100
704	gi12803673	Homo sapiens	, HT002 protein; hypertension-related calcium-regulated gene, clone MGC:3418, mRNA, complete cds.	1129	100
705	gi10435947	Homo sapiens	cDNA FLJ13814 fis, clone THYRO1000368.	3588	99
705	gi3878402	Caenorhabditis elegans	similar to C2 domain	300	25
705	gi3002479	Leishmania major	L3162.1	198	25
706	gi11907998	Homo sapiens	BCL-6 corepressor (BCOR) mRNA, complete cds; alternatively spliced.	2449	100
706	gi7020277	Homo sapiens	cDNA FLJ20285 fis, clone HEP04260.	1131	99
706	gi10432606	Homo sapiens	cDNA FLJ11362 fis, clone HEMBA1000244.	458	50
707	gi7768662	Homo sapiens	C4ST mRNA for chondroitin 4-sulfotransferase, complete cds.	1870	100
707	gi8925966	Homo sapiens	chondroitin 4-O-sulfotransferase 1 mRNA, complete cds.	1870	100
707	gi7572958	Homo sapiens	mRNA for chondroitin-4-sulfotransferase (C4ST gene).	1865	99
708	gi2731561	Homo sapiens	ATP receptor subunit (P2X5) mRNA, complete cds.	2167	96
708	gi1552522	Homo sapiens	Human ionotropic ATP receptor P2X5a mRNA, complete cds.	2131	96
708	gi3387944	Homo sapiens	clone 24793 ionotropic ATP receptor P2X5b mRNA, complete cds.	1608	99
709	gi7021105	Homo sapiens	cDNA FLJ20793 fis, clone COL00343.	1587	100
709	gi7206854	Caenorhabditis elegans	contains similarity to Pfam family PF00085 (Thioredoxins), Score 113, E=9.6e-33, N=1	435	29
709	gi13775331	Caenorhabditis elegans	contains similarity to Pfam family PF00085 (Thioredoxin), score=320.7, E=1.8e-95, N=3	297	28
710	AAV04315	Homo sapiens	Human secreted protein encoded by gene 23.	385	100
710	AAB12155	Homo sapiens	Hydrophobic domain protein isolated from HT-1080 cells.	385	100
711	gi13624098	Homo sapiens	cervical cancer 1 protooncogene protein p40 mRNA, complete cds.	520	100
711	gi12653253	Homo sapiens	, DKFZP586A011 protein, clone MGC:8483, mRNA, complete cds.	520	100
711	gi4886473	Homo sapiens	mRNA; cDNA DKFZp586A011 (from clone DKFZp586A011); partial cds.	520	100
712	gi927415	Homo sapiens	H.sapiens mRNA for carnitine acetyltransferase.	3209	98
712	gi13879380	Mus musculus	Similar to carnitine acetyltransferase	3010	90

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
712	gi758632	Mus musculus	carnitine acetyltransferase	2967	89
713	gi9437507	Homo sapiens	TERA	1198	100
713	gi10439906	Homo sapiens	cDNA: FLJ23279 fis, clone HEP06870.	1198	100
713	gi12652565	Homo sapiens	, TERA protein, clone MGC:1093, mRNA, complete cds.	1198	100
714	gi7023336	Homo sapiens	cDNA FLJ10964 fis, clone PLACE1000748.	1196	100
714	gi14198104	Homo sapiens	, clone MGC:16981, mRNA, complete cds.	1196	100
714	gi7023823	Homo sapiens	cDNA FLJ11269 fis, clone PLACE1009190.	661	100
715	AAB67579	Homo sapiens	Amino acid sequence of a human hydrolytic enzyme HYENZ11.	2740	100
715	gi7020019	Homo sapiens	cDNA FLJ20125 fis, clone COL06152.	1973	99
715	gi13527857	Drosophila melanogaster	pol polyprotein	298	26
716	gi2218077	Homo sapiens	gravin mRNA, complete cds.	8920	99
716	AAW53863	Homo sapiens	Human gravin polypeptide.	8868	99
716	AAB15380	Homo sapiens	Human gravin protein sequence.	8868	99
717	gi7021891	Homo sapiens	cDNA FLJ10060 fis, clone HEMBA1001407.	2306	99
717	gi10433215	Homo sapiens	cDNA FLJ11856 fis, clone HEMBA1006789.	1959	86
717	gi14042890	Homo sapiens	cDNA FLJ14982 fis, clone Y79AA1000258.	1959	86
718	gi6224691	Homo sapiens	Na ⁺ /sulfate cotransporter SUT-1 (SUT-1) mRNA, complete cds.	3271	100
718	AAB36158	Homo sapiens	Novel human transporter protein SEQ ID NO: 2.	3268	99
718	AAB23625	Homo sapiens	Human secreted protein SEQ ID NO: 50.	3268	99
719	gi7020123	Homo sapiens	cDNA FLJ20189 fis, clone COLF0657.	1264	99
719	gi14328904	Homo sapiens	fetal globin-inducing factor (FGIF) mRNA, complete cds.	1262	99
719	AAB71861	Homo sapiens	Human FGIF.	1262	99
720	gi6690250	Homo sapiens	clone HQ0659 PRO0659 mRNA, complete cds.	926	100
720	gi12654109	Homo sapiens	, PRO0659 protein, clone MGC:4888, mRNA, complete cds.	926	100
721	gi608025	Homo sapiens	Human ankyrin G (ANK-3) mRNA, complete cds.	580	32
721	gi3885972	Rattus norvegicus	270 kDa ankyrin G isoform	575	32
721	gi178646	Homo sapiens	Human erythroid ankyrin mRNA, complete cds.	609	35
722	gi7020915	Homo sapiens	cDNA FLJ20666 fis, clone KA1A608.	1229	96
722	gi3169096	Schizosaccharomyces pombe	possible pre-mRNA processing by similarity to yeast prp39	420	37
722	gi1458279	Caenorhabditis elegans	contains similarity to TPR domains	252	29
723	gi7020729	Homo sapiens	cDNA FLJ20548 fis, clone KAT11542.	2200	100
723	gi10434720	Homo sapiens	cDNA FLJ12942 fis, clone NT2RP2005139, weakly similar to 2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-).	2200	100
723	gi11967781	Homo sapiens	ANKRD2 gene for skeletal muscle ankyrin repeat, exons 1-9.	174	30
724	gi10433458	Homo sapiens	cDNA FLJ12068 fis, clone HEMBB1002329.	2903	99
724	gi10434339	Homo sapiens	cDNA FLJ12690 fis, clone	2898	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			NT2RM4002567.		
724	gi10436665	Homo sapiens	cDNA FLJ14252 fis, clone OVARC1001341.	2167	99
725	gi10434638	Homo sapiens	cDNA FLJ12889 fis, clone NT2RP2004098, weakly similar to ADENYLATE CYCLASE (EC 4.6.1.1).	3026	100
725	gi14250313	Homo sapiens	, clone MGC:16864, mRNA, complete cds.	3026	100
725	gi7020356	Homo sapiens	cDNA FLJ20331 fis, clone HEP10410.	1914	99
726	AAAY13947	Homo sapiens	Human transmembrane protein, HP10495.	655	100
726	AAAY07878	Homo sapiens	Human secreted protein fragment encoded from gene 27.	655	100
726	gi6841296	Homo sapiens	HSPC323	449	85
727	gi7159733	Homo sapiens	mRNA for ETAA16 protein.	4318	100
727	AAB10622	Homo sapiens	Human Ewing tumor associated antigen protein.	4318	100
728	gi7020138	Homo sapiens	cDNA FLJ20199 fis, clone COLF1162.	2123	99
728	AAAY91948	Homo sapiens	Human cytoskeleton associated protein 3 (CYSKP-3).	1650	99
728	gi7020210	Homo sapiens	cDNA FLJ20246 fis, clone COLF6458.	1474	99
729	gi13182775	Homo sapiens	CDA11 mRNA, complete cds.	1495	99
729	gi13937914	Homo sapiens	, clone MGC:12519, mRNA, complete cds.	973	97
729	gi2257524	Schizosaccharomyces pombe	HYPOTHETICAL 47.4KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION	536	42
730	gi7020242	Homo sapiens	cDNA FLJ20265 fis, clone COLF9334.	2813	99
730	gi14042159	Homo sapiens	cDNA FLJ14559 fis, clone NT2RM2001998.	2812	99
730	gi499005	Saccharomyces cerevisiae	HRC830	128	32
731	gi7022375	Homo sapiens	cDNA FLJ10379 fis, clone NT2RM2002014.	3182	99
731	gi14010930	Homo sapiens	BAC clone RP11-576F1 from 2, complete sequence.	1868	100
731	gi1573555	Haemophilus influenzae Rd	transcription accessory protein (tex)	691	42
732	gi10434409	Homo sapiens	cDNA FLJ12737 fis, clone NT2RP2000337.	1001	99
733	gi7019597	Homo sapiens	clone PAC 270M7 chromosome 21 map 21q11.2, complete sequence.	5944	100
733	gi7407669	Homo sapiens	chromosome 21 PAC 30P13 map 21q11.2, complete sequence, containing gene for nuclear factor RIP140.	5944	100
733	gi7717256	Homo sapiens	chromosome 21 segment HS21C007.	5944	100
734	gi7021956	Homo sapiens	cDNA FLJ10103 fis, clone HEMBA1002495, weakly similar to LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.	1415	100
734	AAB64828	Homo sapiens	Human secreted protein sequence encoded by gene 12 SEQ ID NO:114.	869	99
734	gi4038594	Lycopersicon esculentum	tDET1 protein	413	37
735	gi6752405	Streptococcus pneumoniae	PspA	137	24
736	gi5080758	Homo sapiens	chromosome 19, BAC 331191 (CIT-B-471E), complete sequence.	1486	55
736	gi456269	Mus musculus domesticus	zinc finger protein 30	1478	54

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
736	gi4567179	Homo sapiens	chromosome 19, BAC 37295 (CIT-B-21A4), complete sequence.	1281	62
737	gi7023220	Homo sapiens	cDNA FLJ10893 fis, clone NT2RP4002791.	4557	99
737	gi14042072	Homo sapiens	cDNA FLJ14507 fis, clone NT2RM1000399.	4439	97
737	gi7582296	Homo sapiens	BM-012	1807	99
738	gi11596985	Homo sapiens	chromosome 14 clone RP11-361H10 map 14q24.3, complete sequence.	1751	100
738	gi7020945	Homo sapiens	cDNA FLJ20689 fis, clone KAlA2890.	1738	99
738	gi6067151	Homo sapiens	chromosome 14 BAC 98L12, complete sequence.	1159	100
739	gi6941888	Homo sapiens	ubiquitin-specific processing protease (USP25) mRNA, complete cds.	5638	99
739	AAB31550	Homo sapiens	A human ubiquitin specific protease (USP).	5638	99
739	gi6693824	Homo sapiens	ubiquitin-specific protease (USP21) mRNA, complete cds.	4022	99
740	gi6693824	Homo sapiens	ubiquitin-specific protease (USP21) mRNA, complete cds.	5465	99
740	AAB31546	Homo sapiens	A human ubiquitin specific protease 25 (USP25).	5465	99
740	AAF24881_aal	Homo sapiens	DNA encoding a human ubiquitin specific protease 25 (USP25).	5465	99
741	gi7161175	Homo sapiens	mRNA for 19A24 protein (19A24 gene).	1726	100
741	gi13021810	Homo sapiens	NK cell receptor (CS1) mRNA, complete cds.	1349	100
741	AAB32373	Homo sapiens	Human secreted protein sequence encoded by gene 3 SEQ ID NO:59.	1349	100
742	gi7023747	Homo sapiens	cDNA FLJ11219 fis, clone PLACE1008122.	2553	100
742	gi7022222	Homo sapiens	cDNA FLJ10287 fis, clone HEMBB1001387.	880	97
742	AAG01392	Homo sapiens	Human secreted protein, SEQ ID NO: 5473.	569	99
743	gi7023747	Homo sapiens	cDNA FLJ11219 fis, clone PLACE1008122.	2442	97
743	gi7022222	Homo sapiens	cDNA FLJ10287 fis, clone HEMBB1001387.	769	89
743	AAG01392	Homo sapiens	Human secreted protein, SEQ ID NO: 5473.	569	99
744	gi6434857	Homo sapiens	pallid mRNA, complete cds.	872	100
744	gi13435969	Homo sapiens	, pallid (mouse) homolog, pallidin, clone MGC:4983, mRNA, complete cds.	872	100
744	gi6456870	Mus musculus	syntaxin 13-interacting protein pallid	754	87
745	gi6841480	Homo sapiens	HSPC129	2378	99
745	gi6841354	Homo sapiens	HSPC058	1825	99
745	gi7022613	Homo sapiens	cDNA FLJ10523 fis, clone NT2RP2000863.	1489	99
746	gi7023644	Homo sapiens	cDNA FLJ11155 fis, clone PLACE1006935.	1826	99
746	AAB18981	Homo sapiens	Amino acid sequence of a human transmembrane protein.	1000	99
746	gi13384531	Caenorhabditis elegans	similar to C. elegans protein T16H12.10	680	40
747	gi13544089	Homo sapiens	, clone IMAGE:4053618, mRNA, partial cds.	2749	99
747	gi6007859	Chlamydomonas reinhardtii	dynein heavy chain alpha	246	30

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
747	gi2065436	Schizosaccharomyces pombe	tealp	227	28
748	gi6650778	Homo sapiens	PRO1575	297	100
749	gi8926849	Homo sapiens	mRNA for Pex3p, complete cds.	1892	99
749	gi4092648	Homo sapiens	mRNA for PEX3 protein, partial.	1892	99
749	gi4218426	Homo sapiens	pex3 gene (joined CDS, promoter and exon 1).	1892	99
750	gi309209	Mus musculus	early B-cell factor	3064	99
750	gi6630994	Homo sapiens	early B-cell transcription factor (EBF) mRNA, partial cds.	3033	98
750	gi7687988	Gallus gallus	early B-cell factor	3023	97
751	gi10436636	Homo sapiens	cDNA FLJ14228 fis, clone NT2RP3004148.	3102	99
751	gi14278861	Homo sapiens	PHD zinc finger transcription factor mRNA, complete cds.	2127	100
751	gi12804495	Homo sapiens	, clone IMAGE:3356959, mRNA, partial cds.	1472	100
752	gi6594639	Homo sapiens	dynein intermediate chain DNAI1 (DNAI1) mRNA, complete cds.	1773	100
752	gi6635422	Homo sapiens	dynein intermediate chain DNAI1 (DNAI1) gene, exon 20 and complete cds.	1768	99
752	gi927637	Anthocidaris crassispina	dynein intermediate chain 2	961	61
753	gi5924385	Rattus norvegicus	ribosomal protein S271	412	100
753	gi12803647	Homo sapiens	, ribosomal protein S27 (metalloprotein 1), clone MGC:3659, mRNA, complete cds.	412	100
753	gi1373421	Homo sapiens	Human ribosomal protein S27 mRNA, complete cds.	412	100
754	gi1655432	Mus musculus	plexin 2	9646	96
754	gi6010215	Homo sapiens	mRNA for partial OCT/plexin-A2 protein.	6985	99
754	gi1665757	Mus musculus	plexin 1	6359	63
755	gi7770189	Homo sapiens	PRO2325	901	100
756	gi7022885	Homo sapiens	cDNA FLJ10697 fis, clone NT2RP3000527, weakly similar to ZINC FINGER PROTEIN 43.	3318	99
756	gi10434872	Homo sapiens	cDNA FLJ13043 fis, clone NT2RP3001338, weakly similar to ZINC FINGER PROTEIN 81.	957	43
756	gi38032	Homo sapiens	Human ZNF43 mRNA.	346	25
757	gi14042238	Homo sapiens	cDNA FLJ14604 fis, clone NT2RP1000363, moderately similar to R.norvegicus LL5 mRNA.	1107	93
757	AAB43723	Homo sapiens	Human cancer associated protein sequence SEQ ID NO:1168.	647	86
757	gi14044043	Homo sapiens	, clone IMAGE:4299555, mRNA, partial cds.	467	66
758	gi7106766	Homo sapiens	HSPC188	532	100
758	gi12804349	Homo sapiens	, clone MGC:4355, mRNA, complete cds.	529	99
758	gi1002516	Saccharomyces cerevisiae	Hgh1p	115	27
759	gi6175593	Homo sapiens	transcription factor IIC90 mRNA, complete cds.	4326	99
760	gi7023345	Homo sapiens	cDNA FLJ10970 fis, clone PLACE1000948.	647	99
760	AAG03409	Homo sapiens	Human secreted protein, SEQ ID NO:	239	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			7490.		
761	gi5441541	Canis familiaris	Ribosomal protein	447	94
761	gi304526	Cricetulus griseus	ribosomal protein S17	447	94
761	gi10439453	Homo sapiens	cDNA: FLJ22917 fis, clone KAT06430.	447	94
762	gi6635353	Homo sapiens	RU1 (RU1) mRNA, complete cds.	4638	99
762	gi8100079	Mus musculus	polycomb-group proteins	4176	88
762	gi8100077	Rattus norvegicus	polycomb-group protein	4152	88
763	gi12804681	Homo sapiens	, S100 calcium-binding protein, beta (neural), clone MGC:1323, mRNA, complete cds.	479	100
763	gi337730	Homo sapiens	Human S100 protein beta-subunit gene, exon 3.	479	100
763	gi404769	Mus musculus	S100 beta protein	473	98
764	gi7106782	Homo sapiens	HSPC196	617	98
764	gi7106786	Homo sapiens	HSPC198	617	98
764	AAW74871	Homo sapiens	Human secreted protein encoded by gene 143 clone HBMDM46.	617	98
765	gi3851206	Homo sapiens	chromosome 19, cosmid F19847, complete sequence.	1282	100
765	gi13276629	Homo sapiens	mRNA; cDNA DKFZp761D221 (from clone DKFZp761D221); complete cds.	815	35
765	gi5701573	Caenorhabditis elegans	similar to S. pombe phosphoprotein (GB:X86179)	430	33
766	gi7020238	Homo sapiens	cDNA FLJ20262 fis, clone COLF7748.	1393	100
766	gi12653607	Homo sapiens	, clone IMAGE:3162218, mRNA, partial cds.	1019	98
766	AAV86358	Homo sapiens	Human gene 11-encoded protein fragment, SEQ ID NO:273.	996	95
767	gi2588619	Homo sapiens	BAC clone CTB-104F4 from 7q21-q22, complete sequence.	2037	100
767	gi1707507	Homo sapiens	H.sapiens mRNA for mitochondrial transcription termination factor.	2037	100
767	gi12654289	Homo sapiens	, transcription termination factor, mitochondrial, clone MGC:5000, mRNA, complete cds.	2033	99
768	gi1314373	Homo sapiens	Human aquaporin-5 (AQP5) gene, exon 4 and complete cds.	1336	100
768	gi664760	Rattus norvegicus	aquaporin-5	1245	91
768	gi4894460	Mus musculus	aquaporin 5	1235	91
769	gi13097624	Homo sapiens	, clone IMAGE:3608084, mRNA, partial cds.	1093	100
769	gi10438279	Homo sapiens	cDNA: FLJ22029 fis, clone HEP08661.	615	60
769	gi13325154	Homo sapiens	, clone IMAGE:3635709, mRNA, partial cds.	609	45
770	AAB48789	Homo sapiens	Human prostate cancer-predisposing protein, CA7 CG04.	2878	100
770	gi11321424	Mus musculus	Ral-A exchange factor RalGPS2	2073	96
770	gi7637906	Homo sapiens	Ral guanine nucleotide exchange factor RalGPS1A mRNA, complete cds.	1224	70
771	gi13623239	Homo sapiens	, Similar to SGC32445 protein, clone MGC:10610, mRNA, complete cds.	1080	99
771	gi7547035	Homo sapiens	SGC32445 protein (SGC32445) mRNA, complete cds.	687	100
771	gi10434977	Homo sapiens	cDNA FLJ13110 fis, clone NT2RP3002549, moderately similar to	519	64

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.		
772	gi13939858	Homo sapiens	RITA	2614	100
772	gi10048470	Homo sapiens	C2H2-like zinc finger protein (ZNF463) mRNA, complete cds.	2614	100
772	gi8575775	Homo sapiens	KRAB zinc finger protein (RITA) mRNA, complete cds.	2614	100
773	gi12654989	Homo sapiens	, clone MGC:5623, mRNA, complete cds.	2300	100
773	gi3329425	Homo sapiens	huntingtin interacting protein HYPE mRNA, partial cds.	963	100
773	gi429189	Haemophilus somnus	surface protein	152	41
774	gi14028017	Mesorhizobium loti	argininosuccinate lyase	199	26
774	gi2182606	Rhizobium sp. NGR234	Y4rH	179	29
775	gi3098311	Oryctolagus cuniculus	elongation factor 1 A2	2410	100
775	gi8886507	Homo sapiens	elongation factor 1 A-2 (EF1A-2) gene, complete cds.	2410	100
775	gi12653327	Homo sapiens	, eukaryotic translation elongation factor 1 alpha 2, clone MGC:8362, mRNA, complete cds.	2410	100
776	gi6624095	Homo sapiens	BAC clone RP11-294L11 from 2, complete sequence.	2515	97
776	AAY66674	Homo sapiens	Membrane-bound protein PRO1277.	2515	97
776	AAB87542	Homo sapiens	Human PRO1277.	2515	97
777	gi6049162	Homo sapiens	rhabdoid tumor deletion region protein 1 (RTDR1) mRNA, complete cds.	1732	100
777	gi14290442	Homo sapiens	, rhabdoid tumor deletion region protein 1, clone MGC:16968, mRNA, complete cds.	1732	100
778	AAB66071	Homo sapiens	Human INTERCEPT 296.	1787	99
778	AAB18992	Homo sapiens	Amino acid sequence of a human transmembrane protein.	880	58
778	AAB26325	Homo sapiens	Human CASB618 protein.	880	58
779	gi643656	Rattus norvegicus	synaptotagmin VII	1851	95
779	gi12667446	Rattus norvegicus	synaptotagmin VII	1851	95
779	gi6136786	Mus musculus	synaptotagmin VII	1842	95
780	gi7020988	Homo sapiens	cDNA FLJ20716 fis, clone HEP19742.	1048	100
780	gi4033606	Adiantum capillus-veneris	Extensin	131	38
780	gi169347	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	130	38
781	gi7020477	Homo sapiens	cDNA FLJ20401 fis, clone KAT00901.	1644	96
781	gi7022002	Homo sapiens	cDNA FLJ10135 fis, clone HEMBA1003117.	590	40
781	gi7022284	Homo sapiens	cDNA FLJ10324 fis, clone NT2RM2000567.	590	40
782	gi6808186	Homo sapiens	mRNA; cDNA DKFZp434D0218 (from clone DKFZp434D0218); partial cds.	1322	99
783	gi505544	Homo sapiens	H.sapiens mRNA for Zinc-finger protein (ZNFpT1).	1211	99
783	AAY58627	Homo sapiens	Protein regulating gene expression PRGE-20.	688	50
783	gi9187356	Homo sapiens	mRNA full length insert cDNA clone	687	50

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			EUROIMAGE 2107395.		
784	gi8896094	Homo sapiens	SH3-containing protein SH3GLB2 mRNA, complete cds.	1975	97
784	gi4929591	Homo sapiens	CGI-61 protein mRNA, complete cds.	706	69
784	gi8896092	Homo sapiens	SH3-containing protein SH3GLB1 mRNA, complete cds.	706	69
785	gi7770175	Homo sapiens	PRO2249	1827	99
785	gi11527602	Homo sapiens	mRNA for MCM10 homolog, complete cds.	1827	99
785	gi12053187	Homo sapiens	mRNA; cDNA DKFZp434H152 (from clone DKFZp434H152); complete cds.	1682	99
786	gi7023364	Homo sapiens	cDNA FLJ10982 fis, clone PLACE1001692, moderately similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14).	1413	99
786	gi7023563	Homo sapiens	cDNA FLJ11106 fis, clone PLACE1005763, moderately similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14).	1099	98
786	gi205326	Rattus norvegicus	S-acyl fatty acid synthetase thio ester hydrolase, medium chain	807	55
787	gi2599502	Homo sapiens	protocadherin 68 (PCH68) mRNA, complete cds.	327	43
787	AAAY24913	Homo sapiens	Human ontherin.	327	43
787	AAAY94991	Homo sapiens	Human secreted protein vc35_1, SEQ ID NO:22.	296	28
788	gi7023688	Homo sapiens	cDNA FLJ11183 fis, clone PLACE1007488, weakly similar to PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR.	2260	100
788	gi3342246	Rattus norvegicus	actin-filament binding protein Frabin	725	32
788	gi595425	Homo sapiens	Human faciogenital dysplasia (FGD1) mRNA, complete cds.	759	32
789	gi6554165	Homo sapiens	receptor protein tyrosine phosphatase (RPTP-rho) mRNA, alternatively spliced, complete cds.	7734	99
789	gi13378306	Mus musculus	brain RPTPmam4 isoform I	7499	97
789	gi32456	Homo sapiens	H.sapiens hR-PTPu gene for protein tyrosine phosphatase.	4995	64
790	gi7020479	Homo sapiens	cDNA FLJ20402 fis, clone KAT00919.	2024	99
790	gi7770205	Homo sapiens	PRO2521	1957	97
790	gi10241843	Mus musculus	gasdermin	282	29
791	gi5262472	Homo sapiens	mRNA; cDNA DKFZp564J102 (from clone DKFZp564J102); partial cds.	1602	100
792	gi10436457	Homo sapiens	cDNA FLJ14084 fis, clone HEMBB1002383.	830	100
792	AAAY94940	Homo sapiens	Human secreted protein clone yi62_1 protein sequence SEQ ID NO:86.	830	100
792	AAAY57922	Homo sapiens	Human transmembrane protein HTMPN-46.	830	100
793	gi7328061	Homo sapiens	mRNA; cDNA DKFZp761I2312 (from clone DKFZp761I2312); partial cds.	2723	100
793	gi14039825	Mus musculus	gamma-1 syntrophin	2579	93
793	gi8247279	Homo sapiens	mRNA for syntrophin 4.	2271	97
794	gi6164674	Homo sapiens	heterogeneous nuclear ribonucleoprotein, alternate transcript (RALY) mRNA,	730	66

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			complete cds.		
794	gi14250048	Homo sapiens	, heterogeneous nuclear ribonucleoprotein C (C1/C2), clone MGC:14574, mRNA, complete cds.	705	53
794	gi13937888	Homo sapiens	, Similar to heterogeneous nuclear ribonucleoprotein C, clone MGC:12469, mRNA, complete cds.	704	53
795	gi12653905	Homo sapiens	, Similar to Max dimerization protein 3, clone MGC:2383, mRNA, complete cds.	1045	100
795	AAV93137	Homo sapiens	Human Myx protein.	1023	98
795	AAB35713	Homo sapiens	Human Mad3 protein sequence.	1010	97
796	gi7020704	Homo sapiens	cDNA FLJ20533 fis, clone KAT10931.	585	98
797	gi1106878	Homo sapiens	HSPC244	398	98
797	AAV07855	Homo sapiens	Human secreted protein fragment encoded from gene 4.	398	98
797	gi13274582	Mus musculus	thymus atrophy-related protein	383	95
798	gi8886483	Gallus gallus	EURL	1178	74
798	gi10435877	Homo sapiens	cDNA FLJ13763 fis, clone PLACE4000089.	873	98
798	AAG01108	Homo sapiens	Human secreted protein, SEQ ID NO: 5189.	561	100
799	AAV33297	Homo sapiens	Human membrane spanning protein MSP-4.	781	100
799	AAB61149	Homo sapiens	Human NOV18 protein.	781	100
799	AAB61150	Homo sapiens	Human NOV19 protein.	781	100
800	gi8099348	Homo sapiens	zinc finger protein (ZFP) mRNA, complete cds.	4066	99
800	gi2293535	Homo sapiens	zinc finger protein (ZnF20) mRNA, complete cds.	1863	49
800	gi11527849	Mus musculus	zinc finger protein SKAT2	1323	58
801	gi7023523	Homo sapiens	cDNA FLJ11082 fis, clone PLACE1005206.	2693	99
801	gi9558010	Leishmania major	possible cDNA flj11082 fis, clone place1005206	134	26
802	gi6841558	Homo sapiens	HSPC168	1502	100
802	gi6453346	Homo sapiens	Novel human gene on chromosome 20.	1502	100
802	gi13542748	Mus musculus	RIKEN cDNA 3230401D17 gene	1314	86
803	gi7020468	Homo sapiens	cDNA FLJ20396 fis, clone KAT00561.	931	100
803	AAB18980	Homo sapiens	Amino acid sequence of a human transmembrane protein.	931	100
803	AAV91632	Homo sapiens	Human secreted protein sequence encoded by gene 25 SEQ ID NO:305.	914	98
804	gi6650345	Homo sapiens	alpha-catenin-like protein VR22 mRNA, complete cds.	4478	99
804	gi222788	Gallus gallus	alpha N-catenin	2765	60
804	AAR58778	Homo sapiens	Neural alpha-catenin protein.	2765	60
805	gi10434911	Homo sapiens	cDNA FLJ13068 fis, clone NT2RP3001739, weakly similar to HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.	587	38
805	gi5912258	Homo sapiens	mRNA; cDNA DKFZp586K0524 (from clone DKFZp586K0524); partial cds.	190	41
805	gi7022673	Homo sapiens	cDNA FLJ10562 fis, clone NT2RP2002701.	154	44
806	gi10435877	Homo sapiens	cDNA FLJ13763 fis, clone PLACE4000089.	876	99
806	gi8886483	Gallus gallus	EURL	868	72
806	AAG01108	Homo sapiens	Human secreted protein, SEQ ID NO: 5189.	561	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
807	gi4521254	Mus musculus	cornichon-like protein	867	100
807	AAB60464	Homo sapiens	Human cell cycle and proliferation protein CCYPR-12, SEQ ID NO:12.	729	81
807	AAY76218	Homo sapiens	Human secreted protein encoded by gene 95.	716	81
808	gi7407144	Homo sapiens	protocadherin Fat 2 (FAT2) mRNA, complete cds.	22667	99
808	gi3449286	Rattus norvegicus	MEGF1	18806	81
808	gi6688786	Mus musculus	mouse fat 1 cadherin	8928	47
809	gi7407144	Homo sapiens	protocadherin Fat 2 (FAT2) mRNA, complete cds.	19770	99
809	gi3449286	Rattus norvegicus	MEGF1	16567	82
809	gi6688786	Mus musculus	mouse fat 1 cadherin	8928	47
810	gi7020201	Homo sapiens	cDNA FLJ20241 fis, clone COLF6335.	2420	100
810	gi10435321	Homo sapiens	cDNA FLJ13337 fis, clone OVARC1001880.	1279	99
810	gi7020600	Homo sapiens	cDNA FLJ20475 fis, clone KAT07206.	634	60
811	gi6483290	Homo sapiens	CDH7 mRNA for cadherin-7, complete cds.	4032	100
811	gi10803408	Homo sapiens	mRNA for cadherin-7 (CDH7 gene).	3965	98
811	gi868001	Gallus gallus	chicken cadherin-7	3830	93
812	gi13276621	Homo sapiens	mRNA; cDNA DKFZp761G1913 (from clone DKFZp761G1913).	1204	97
812	gi8977983	Mus musculus	neuronal interacting factor X 1 (NIX1)	699	78
812	gi10437116	Homo sapiens	cDNA: FLJ21097 fis, clone CAS03931.	297	42
814	gi13279269	Homo sapiens	, clone IMAGE:3631943, mRNA, partial cds.	1480	100
814	gi6808028	Homo sapiens	mRNA; cDNA DKFZp761C029 (from clone DKFZp761C029); partial cds.	857	100
814	AAW88657	Homo sapiens	Secreted protein encoded by gene 124 clone HPMCJ92.	436	94
815	gi7959853	Homo sapiens	PRO1966	281	100
816	gi7259234	Mus musculus	contains transmembrane (TM) region	718	65
816	AAY94954	Homo sapiens	Human secreted protein clone iw66_1 protein sequence SEQ ID NO:114.	679	58
816	AAB62810	Homo sapiens	Human nervous system associated protein NSPRT3 amino acid sequence.	678	61
817	gi5921144	Schizosaccharomyces pombe	mip1	1489	48
817	gi458938	Saccharomyces cerevisiae	Yhr186cp	469	30
817	gi9366720	Trypanosoma brucei	possible t16o11.22 protein.	277	45
819	gi7020799	Homo sapiens	cDNA FLJ20590 fis, clone KAT09052.	727	100
820	gi7020555	Homo sapiens	cDNA FLJ20449 fis, clone KAT05575.	1857	99
820	AAY79269	Homo sapiens	Human testis-specific transcription factor PHELIX.	1696	99
821	gi6482350	Homo sapiens	CAC-1 mRNA, partial cds.	1136	100
821	gi13937595	Homo sapiens	, Similar to RIKEN cDNA 1810017F10 gene, clone MGC:2583, mRNA, complete cds.	560	94
821	AAY25770	Homo sapiens	Human secreted protein encoded from gene 60.	560	94
822	gi10434608	Homo sapiens	cDNA FLJ12871 fis, clone NT2RP2003751.	2023	100
822	gi6093227	Homo sapiens	mRNA; cDNA DKFZp434I0850 (from clone DKFZp434I0850); partial cds.	1607	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
822	gi6453452	Homo sapiens	mRNA; cDNA DKFZp434L0850 (from clone DKFZp434L0850).	1607	100
823	AAV13402	Homo sapiens	Amino acid sequence of protein PRO310.	1079	63
823	AAB18988	Homo sapiens	Amino acid sequence of a human transmembrane protein.	1079	63
823	AAB80270	Homo sapiens	Human PRO310 protein.	1079	63
824	gi13938181	Homo sapiens	, clone IMAGE:2905978, mRNA, partial cds.	2722	99
824	gi6453540	Homo sapiens	mRNA; cDNA DKFZp434D0428 (from clone DKFZp434D0428); partial cds.	2455	99
824	gi10440436	Homo sapiens	mRNA for FLJ00053 protein, partial cds.	807	100
825	gi7022318	Homo sapiens	cDNA FLJ10346 fis, clone NT2RM2001004.	1475	100
826	gi7110152	Mus musculus	selenocysteine lyase SCLY	1219	80
826	gi7022600	Homo sapiens	cDNA FLJ10515 fis, clone NT2RP2000764, weakly similar to NIFS PROTEIN.	592	98
826	gi9887215	Methanosarcina thermophila	cysteine desulfurase NifS	315	43
827	gi7022560	Homo sapiens	cDNA FLJ10491 fis, clone NT2RP2000239.	1266	100
827	gi7022033	Homo sapiens	cDNA FLJ10156 fis, clone HEMBA1003447.	1161	97
828	gi8247250	Homo sapiens	mRNA for neutral sphingomyelinase II (nSMase2 gene).	3489	100
828	AAB70772	Homo sapiens	Human neutral cerebral sphingomyelinase protein.	3489	100
828	gi8247281	Mus musculus	neutral sphingomyelinase II	3187	91
829	gi7020945	Homo sapiens	cDNA FLJ20689 fis, clone KAIA2890.	2459	100
829	gi11596985	Homo sapiens	chromosome 14 clone RP11-361H10 map 14q24.3, complete sequence.	1819	97
829	gi6067151	Homo sapiens	chromosome 14 BAC 98L12, complete sequence.	1153	99
830	gi10039443	Homo sapiens	NEDL1 mRNA for NEDD4-like ubiquitin ligase 1, complete cds.	4335	56
830	AAW93167	Homo sapiens	Human ZGGBP1 protein.	992	47
830	gi1374782	Mus musculus	possible ubiquitin protein ligase	1062	50
831	gi7021974	Homo sapiens	cDNA FLJ10115 fis, clone HEMBA1002777.	1882	99
831	gi7021027	Homo sapiens	cDNA FLJ20739 fis, clone HEP07341.	1252	98
831	gi5002381	Takifugu rubripes	BAW	776	72
832	gi7022523	Homo sapiens	cDNA FLJ10469 fis, clone NT2RP2000008, weakly similar to ZINC FINGER PROTEIN 84.	3772	99
832	gi1020145	Homo sapiens	Human DNA binding protein (HPF2) mRNA, complete cds.	1714	48
832	gi7243633	Homo sapiens	RB-associated KRAB repressor (RBAK) mRNA, complete cds.	1653	46
833	gi6433864	Homo sapiens	CLDN12 gene for claudin-12.	1295	100
833	gi12053057	Homo sapiens	mRNA; cDNA DKFZp434I1816 (from clone DKFZp434I1816); complete cds.	1295	100
833	gi9799020	Mus musculus	claudin-12	1125	91
834	gi12053151	Homo sapiens	mRNA; cDNA DKFZp434G0326 (from clone DKFZp434G0326); complete cds.	5605	99
834	gi7020102	Homo sapiens	cDNA FLJ20176 fis, clone COL09928.	1268	88
834	gi7023725	Homo sapiens	cDNA FLJ11205 fis, clone PLACE1007843.	719	100
835	gi7020789	Homo sapiens	cDNA FLJ20583 fis, clone KAT09685.	2153	99

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
835	AAG02503	Homo sapiens	Human secreted protein, SEQ ID NO: 6584.	423	98
835	gi14289183	Homo sapiens	chac mRNA for chorein, complete cds.	193	24
836	gi7022600	Homo sapiens	cDNA FLJ10515 fis, clone NT2RP2000764, weakly similar to NIFS PROTEIN.	1301	100
836	gi7110152	Mus musculus	selenocysteine lyase SCLY	1107	83
836	gi13592392	Caenorhabditis elegans	Contains similarity to Pfam domain: PF00266 (aminotran_5), Score=51.6, E-value=5.7e-12, N=1	468	44
837	gi7274380	Homo sapiens	group III secreted phospholipase A2 mRNA, complete cds.	2813	99
837	gi4314431	Homo sapiens	PAC clone RP3-412A9 from 22, complete sequence.	596	99
837	gi5627	Apis mellifera	phospholipase A-2	243	41
838	gi8331760	Homo sapiens	X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein (ALD), plexin-related protein (PLXB3), muscle-specific serine kinase (MSSK), NAD-isocitrate dehydrogenase (IDH), translocon-associated protein delta (TRAP), and LU1 protein (LU1) genes, complete cds; and CCp pseudogene, complete sequence.	3242	100
838	gi6651019	Mus musculus	semaphorin cytoplasmic domain-associated protein 3A	1583	50
838	gi6651021	Mus musculus	semaphorin cytoplasmic domain-associated protein 3B	1583	50
839	gi7023290	Homo sapiens	cDNA FLJ10932 fis, clone OVARC1000588.	718	100
840	gi6094681	Homo sapiens	PAC clone RP5-1049N15 from 7q31.2-7q32, complete sequence.	4804	100
840	gi7264724	Homo sapiens	alpha-aminoadipate semialdehyde synthase mRNA, complete cds.	4804	100
840	gi4938304	Homo sapiens	mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase, partial CDS.	4799	99
841	AAAY66700	Homo sapiens	Membrane-bound protein PRO1137.	1164	95
841	AAB65223	Homo sapiens	Human PRO1137 (UNQ575) protein sequence SEQ ID NO:250.	1164	95
841	AAAY50917	Homo sapiens	Human fetal brain cDNA clone vc4_1 derived protein.	1023	100
842	AAW56477	Homo sapiens	Amino acid sequence of human bone morphogenetic protein-16 (BMP-16).	1183	100
842	AAAY03849	Homo sapiens	Human nodal protein.	1183	100
842	gi296605	Mus musculus	nodal	986	84
843	gi7020399	Homo sapiens	cDNA FLJ20356 fis, clone HEP15821.	5470	100
843	gi10435659	Homo sapiens	cDNA FLJ13605 fis, clone PLACE1010562.	224	44
844	gi4886471	Homo sapiens	mRNA; cDNA DKFZp586N0819 (from clone DKFZp586N0819).	531	100
845	gi3288470	Homo sapiens	surf5c mRNA, clone 10.9.	728	100
845	gi3288452	Homo sapiens	Surf-5 and Surf-6 genes.	334	94
845	gi3288468	Homo sapiens	surf5b mRNA, clone L5.	334	94
846	gi14149050	Drosophila	turtle protein, isoform 4	1037	32

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
		melanogaster			
846	gi14149048	Drosophila melanogaster	turtle protein, isoform 3	1037	32
846	gi14149046	Drosophila melanogaster	turtle protein, isoform 2	939	34
847	gi7021049	Homo sapiens	cDNA FLJ20753 fis, clone HEP02714.	2930	99
847	gi9886896	Human herpesvirus 8	Orf73	175	20
847	gi11037008	Human herpesvirus 8	latent nuclear antigen	172	20
848	gi12597293	Homo sapiens	acidic mammalian chitinase precursor, mRNA, complete cds.	2018	100
848	gi6467177	Homo sapiens	TSA1902-L mRNA for novel member of chitinase family, complete cds.	2010	99
848	gi6467179	Homo sapiens	TSA1902-S mRNA for novel member of chitinase family, complete cds.	1725	99
849	gi32391	Homo sapiens	Human HOX4C mRNA for a homeobox protein.	1802	98
849	gi51416	Mus musculus	Hox-4.4	1591	88
849	gi4322104	Danio rerio	homeobox protein	425	82
850	gi1359443	Homo sapiens	Human gene for hepatitis C-associated microtubular aggregate protein p44, exon 9 and complete cds.	2299	99
850	AAV05371	Homo sapiens	Human HCMV inducible gene protein, SEQ ID NO 10.	2299	99
850	gi218576	Pan troglodytes	p44	2242	97
851	gi575494	Homo sapiens	MHC class II lymphocyte antigen beta-chain (HLA-DPB1a) mRNA, complete cds.	437	72
851	gi188479	Homo sapiens	Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds.	437	72
851	gi14044082	Homo sapiens	, Similar to major histocompatibility complex, class II, DP beta 1, clone MGC:14112, mRNA, complete cds.	429	70
852	gi181547	Homo sapiens	defensin 6 mRNA, complete cds.	318	90
852	AAR44819	Homo sapiens	Sequence of the gastrointestinal defensin (GID) peptide called human defensin 6.	318	90
852	gi1200182	Homo sapiens	Human defensin 6 (HD-6) gene, complete cds.	314	89
853	gi13396914	Homo sapiens	The gene of C2GnT3	2389	100
853	gi7527464	Homo sapiens	core 2 beta-1,6-N-acetylglucosaminyltransferase 3 (C2GnT3) mRNA, complete cds.	2389	100
853	AAU00037	Homo sapiens	Human C2GnT3.	2389	100
855	gi7959772	Homo sapiens	PRO1483	252	100
856	gi5911169	Homo sapiens	transmembrane mucin 12 (MUC12) mRNA, partial cds.	2914	99
856	AAV59290	Homo sapiens	Human MUC12 polypeptide.	2914	99
856	gi2589172	Rattus norvegicus	mucin Muc3	595	36
857	AAE00508	Homo sapiens	Human lipase protein, MLip-1.	1456	100
857	gi56600	Rattus norvegicus	triacylglycerol lipase	776	58
857	gi3108175	Mus musculus	pancreatic lipase related protein 1	772	57
858	AAV94954	Homo sapiens	Human secreted protein clone iw66_1 protein sequence SEQ ID NO:114.	1112	100
858	gi10434269	Homo sapiens	cDNA FLJ12650 fis, clone	872	100

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			NT2RM4002054.		
858	gi7259234	Mus musculus	contains transmembrane (TM) region	660	60
859	gi7021851	Homo sapiens	cDNA FLJ10035 fis, clone HEMBA1000919.	1589	100
859	gi10440420	Homo sapiens	mRNA for FLJ00045 protein, partial cds.	654	89
859	AA999671	Homo sapiens	Human GTPase associated protein-22.	654	89
860	gi7022523	Homo sapiens	cDNA FLJ10469 fis, clone NT2RP2000008, weakly similar to ZINC FINGER PROTEIN 84.	3573	99
860	gi1020145	Homo sapiens	Human DNA binding protein (HPF2) mRNA, complete cds.	1604	48
860	gi12584159	Homo sapiens	zinc finger protein 268 (ZNF268) mRNA, complete cds.	1542	48
861	gi6539434	Homo sapiens	SPR1 mRNA, complete cds.	808	100
861	gi6523547	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	185	39
861	gi904359	Beta vulgaris	chitinase 1	185	41
862	gi7021924	Homo sapiens	cDNA FLJ10081 fis, clone HEMBA1002018.	2742	100
862	gi10435862	Homo sapiens	cDNA FLJ13751 fis, clone PLACE3000339, weakly similar to GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3).	2687	99
862	gi1275988	Homo sapiens	testis development protein PRTD mRNA, complete cds.	2454	99
863	gi7019913	Homo sapiens	cDNA FLJ20060 fis, clone COL01358.	1830	100
863	gi10434817	Homo sapiens	cDNA FLJ13006 fis, clone NT2RP3000449.	1823	99
863	gi10434659	Homo sapiens	cDNA FLJ12902 fis, clone NT2RP2004347.	1724	99
864	gi7329718	Homo sapiens	Novel human gene mapping to chromosome 1.	11682	99
864	gi7022765	Homo sapiens	cDNA FLJ10619 fis, clone NT2RP2005472.	3153	99
864	gi14388939	Homo sapiens	chorea-acanthocytosis (CHAC) mRNA, complete cds.	462	30
865	gi28971	Homo sapiens	H.sapiens mRNA for autoantigen NOR-90.	3813	100
865	gi509241	Homo sapiens	Human mRNA for upstream binding factor (hUBF).	2661	78
865	AAB44430	Homo sapiens	Human lung tumour-specific antigen encoded by cDNA	2649	78
866	gi13445482	Homo sapiens	HP43.8KD mRNA, complete cds.	282	47
866	gi10434108	Homo sapiens	cDNA FLJ12552 fis, clone NT2RM4000712, moderately similar to Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA.	219	36
866	gi10436670	Homo sapiens	cDNA FLJ14256 fis, clone PLACE1000007, weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15).	219	36
867	AAB73229	Homo sapiens	Human phosphatase MTMR7 h.	743	57
867	gi5901814	Drosophila melanogaster	BcDNA.GH04637	503	48
867	gi7020021	Homo sapiens	cDNA FLJ20126 fis, clone COL06160.	697	73
868	gi7959801	Homo sapiens	PRO0800	392	100
869	gi12654971	Homo sapiens	, calcium-regulated heat-stable protein (24kD), clone MGC:5586, mRNA,	417	97

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			complete cds.		
869	gi13097198	Homo sapiens	, calcium-regulated heat-stable protein (24kD), clone MGC:5235, mRNA, complete cds.	417	97
869	AAW61023	Homo sapiens	Human RNA binding protein.	417	97
870	gi6650832	Homo sapiens	PRO2086	243	100
871	gi2217942	Rattus norvegicus	glycoprotein specific UDP-glucuronyltransferase	1802	97
871	gi8051678	Homo sapiens	hu-GlcAT-P mRNA for glucuronyltransferase, complete cds.	1757	99
871	gi4519214	Rattus norvegicus	UDP-glucuronyltransferase-S	760	50
872	gi14286288	Homo sapiens	, Similar to RIKEN cDNA 2010004P11 gene, clone MGC:2734, mRNA, complete cds.	715	100
872	gi13529665	Mus musculus	RIKEN cDNA 2010004P11 gene	706	98
872	gi2565364	Musca domestica	Sex-lethal protein	134	33
873	gi190406	Homo sapiens	Human profilaggrin gene exons 1-3, 5' end.	6301	99
873	gi190396	Homo sapiens	Human profilaggrin gene, 3' end.	5133	99
873	gi190404	Homo sapiens	Human profilaggrin mRNA, 3' end.	3696	89
874	gi791002	Homo sapiens	ARSD gene, complete CDS.	1761	99
874	gi6651286	Homo sapiens	arylsulfatase D beta (ARSD) mRNA, complete cds.	1756	99
874	gi791004	Homo sapiens	ARSE gene, complete CDS.	947	58
875	gi13097675	Homo sapiens	, Similar to uncharacterized hypothalamus protein HCDASE, clone MGC:1171, mRNA, complete cds.	612	96
875	AAV87599	Homo sapiens	Human fatty acid beta-oxidation enzyme HUFA-2.	612	96
875	AAG03352	Homo sapiens	Human secreted protein, SEQ ID NO: 7433.	591	100
876	gi6180180	Homo sapiens	transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel alpha-1 subunit gene, partial cds, complete sequence.	908	100
876	gi3114826	Homo sapiens	mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLC110F1857Q7 (RZPD Berlin)).	908	100
876	gi7673612	Mus musculus	DXImx39e protein	831	91
877	gi13543663	Homo sapiens	, ubiquitin-conjugating enzyme E2D 1 (homologous to yeast UBC4/5), clone MGC:14673, mRNA, complete cds.	805	100
877	gi460810	Homo sapiens	H.sapiens UBCH5 mRNA for ubiquitin conjugating enzyme.	805	100
877	gi4868140	Homo sapiens	ubiquitin-conjugating enzyme HBUCE1 mRNA, complete cds.	747	91
878	gi7020915	Homo sapiens	cDNA FLJ20666 fis, clone KAIA608.	1288	100
878	gi3169096	Schizosaccharomyces pombe	possible pre-mRNA processing by similarity to yeast prp39	279	33
878	gi10177721	Arabidopsis thaliana	gene_id:MPL12.20~	146	22
879	gi7020681	Homo sapiens	cDNA FLJ20519 fis, clone KAT10365.	891	100
879	AAV87267	Homo sapiens	Human signal peptide containing protein	824	95

SEQ ID NO:	Accession No.	Species	Description	Score	% Identity
			HSPP-44 SEQ ID NO:44.		
879	AAB65245	Homo sapiens	Human PRO1104 (UNQ547) protein sequence SEQ ID NO:297.	824	95
880	gi6560622	Homo sapiens	PRO0611	501	100
881	AAB57079	Homo sapiens	Human prostate cancer antigen protein sequence SEQ ID NO:1657.	668	100
881	AAAY99372	Homo sapiens	Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116.	668	100
881	AAB88356	Homo sapiens	Human membrane or secretory protein clone PSEC0082.	661	99
882	gi1381181	Oryctolagus cuniculus	ubiquitin-conjugating enzyme E2-32k	663	100
882	gi13436071	Homo sapiens	, clone MGC:10481, mRNA, complete cds.	663	100
882	gi7020506	Homo sapiens	cDNA FLJ20419 fis, clone KAT02435.	658	99
883	gi1381181	Oryctolagus cuniculus	ubiquitin-conjugating enzyme E2-32k	1265	99
883	gi13436071	Homo sapiens	, clone MGC:10481, mRNA, complete cds.	1265	99
883	gi7020506	Homo sapiens	cDNA FLJ20419 fis, clone KAT02435.	1256	98
884	gi1381181	Oryctolagus cuniculus	ubiquitin-conjugating enzyme E2-32k	383	97
884	gi13436071	Homo sapiens	, clone MGC:10481, mRNA, complete cds.	383	97
884	gi7020506	Homo sapiens	cDNA FLJ20419 fis, clone KAT02435.	383	97
885	gi14424536	Homo sapiens	, Similar to septin 6, clone MGC:16619, mRNA, complete cds.	2183	99
885	gi5689158	Mus musculus	Septin6	2114	95
885	gi7023141	Homo sapiens	cDNA FLJ10849 fis, clone NT2RP4001414, highly similar to SEPTIN 2 HOMOLOG.	1840	82
886	gi14424536	Homo sapiens	, Similar to septin 6, clone MGC:16619, mRNA, complete cds.	1213	63
886	gi5689158	Mus musculus	Septin6	1162	62
886	gi7023141	Homo sapiens	cDNA FLJ10849 fis, clone NT2RP4001414, highly similar to SEPTIN 2 HOMOLOG.	995	51
887	gi4309951	Homo sapiens	BAC clone RP11-121A8 from 7p14-p13, complete sequence.	684	100
887	AAG00417	Homo sapiens	Human secreted protein, SEQ ID NO: 4498.	684	100
887	gi339159	Homo sapiens	Human T-cell receptor germline gamma-chain gene V-region (V3; subgroup I).	392	73
888	gi2570015	Homo sapiens	H.sapiens PAX7 gene, exon 1 (and joined CDS).	2756	100
888	gi2570021	Homo sapiens	H.sapiens mRNA for paired box containing transcription factor, PAX7.	2756	100
888	gi2570014	Homo sapiens	H.sapiens PAX7 gene, exon 1 (and joined CDS).	2735	99

TABLE 3

SEQ ID NO:	Accession No.	Description	Results*
445	BL00434	HSF-type DNA-binding domain proteins.	BL00434C 23.85 7.111e-09 1089-1129
446	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.000e-13 216-229 PD00066 13.92 2.286e-12 244-257 PD00066 13.92 4.522e-11 299-312 PD00066 13.92 6.538e-10 157-170 PD00066 13.92 7.923e-10 327-340
453	PR00037	LACR BACTERIAL REGULATORY PROTEIN HTH SIGNATURE	PR00037A 12.66 6.786e-09 34-49
465	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 6.100e-09 197-212 PR00320C 13.01 6.400e-09 393-408 PR00320A 16.74 8.683e-09 197-212 PR00320B 12.19 9.775e-09 299-314
466	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 5.881e-09 14-47
470	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175D 27.67 8.500e-40 175-227 BL00175C 23.75 5.000e-25 90-122 BL00175A 15.42 8.333e-20 17-37 BL00175B 12.60 1.000e-12 66-79
472	BL00315	Dehydrins proteins.	BL00315A 9.35 8.119e-09 105-133
473	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.000e-11 44-53
475	PD02448	TRANSCRIPTION PROTEIN DNA-BINDIN.	PD02448A 9.37 4.293e-09 171-210
477	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625A 12.84 8.500e-19 121-141 PR00625B 13.48 3.204e-15 151-172
478	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 5.853e-10 26-70
479	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.706e-11 49-62
480	PR00501	KELCH REPEAT SIGNATURE	PR00501A 8.25 9.182e-09 544-558
483	PR00878	CHOLINESTERASE SIGNATURE	PR00878F 5.37 5.179e-12 500-513
484	BL00378	Hexokinases proteins.	BL00378C 16.14 1.000e-40 207-251 BL00378E 22.92 1.000e-40 725-771 BL00378C 16.14 3.520e-40 655-699 BL00378E 22.92 3.382e-36 277-323 BL00378B 14.23 5.333e-35 509-546 BL00378B 14.23 8.953e-28 61-98 BL00378A 19.01 1.346e-22 22-50 BL00378F 8.27 2.688e-17 893-908 BL00378D 10.94 6.294e-17 703-715 BL00378D 10.94 5.500e-16 255-267 BL00378F 8.27 9.609e-13 445-460 BL00378A 19.01 3.017e-12 470-498
485	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.688e-15 352-369 BL00028 16.07 4.375e-15 324-341 BL00028 16.07 4.176e-14 604-621 BL00028 16.07 8.412e-14 380-397 BL00028 16.07 9.471e-14 576-593 BL00028 16.07 1.450e-13 548-565 BL00028 16.07 2.350e-13 436-453 BL00028 16.07 4.150e-13 492-509 BL00028 16.07 5.050e-13 296-313 BL00028 16.07 1.783e-12 520-537

SEQ ID NO:	Accession No.	Description	Results*
			BL00028 16.07 3.348e-12 632-649 BL00028 16.07 5.304e-12 408-425 BL00028 16.07 5.304e-12 660-677 BL00028 16.07 4.808e-11 464-481 BL00028 16.07 7.000e-10 268-285
486	BL00301	GTP-binding elongation factors proteins.	BL00301B 20.09 1.429e-26 128-160 BL00301A 12.41 6.400e-15 62-74
487	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 7.600e-12 826-837
489	BL00227	Tubulin subunits alpha, beta, and gamma proteins.	BL00227B 19.29 1.000e-40 52-107 BL00227C 25.48 1.000e-40 113-165 BL00227D 18.46 1.000e-40 222-276 BL00227F 21.16 1.000e-40 382-436 BL00227E 24.15 6.727e-36 326-361 BL00227A 24.55 2.125e-33 1-35
490	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.625e-09 1271-1287
491	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.625e-09 1250-1266
492	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 5.500e-19 138-169 BL00107B 13.31 1.000e-16 203-219
493	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 5.000e-15 392-411 BL50002B 15.18 2.500e-09 430-444
494	PR00049	WILMS TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.949e-09 87-102
497	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 6.172e-09 249-299
498	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-16 362-375 PD00066 13.92 4.462e-15 334-347 PD00066 13.92 8.615e-15 473-486 PD00066 13.92 5.200e-14 306-319 PD00066 13.92 3.000e-13 390-403
500	PF00780	Domain found in NIK1-like kinases, mouse citron and yeast ROM.	PF00780I 14.69 7.863e-09 293-323
501	BL00518	Zinc finger, C3HC4 type (RING finger), proteins:	BL00518 12.23 7.333e-09 279-288
502	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418A 20.83 2.050e-23 1537-1585 DM01418B 22.51 5.895e-21 1632-1674 DM01418C 20.48 8.571e-18 1702-1744
508	BL01052	Calponin family repeat proteins.	BL01052B 15.31 1.000e-09 131-157
512	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 7.107e-36 27-63
515	DM00475	w LOW TRANSPOSASE SAPA 12K.	DM00475B 12.12 6.019e-09 386-406
516	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.865e-11 64-81
519	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625A 12.84 2.019e-14 76-96 PR00625B 13.48 5.714e-11 106-127
520	BL00216	Sugar transport proteins.	BL00216B 27.64 6.400e-10 92-142
523	BL01033	Globins profile.	BL01033B 13.81 1.000e-15 38-50
526	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 4.750e-12 1075-1089
531	PR00249	SECRETIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00249G 15.72 8.892e-10 387-409 PR00249C 17.08 6.609e-09 223-247
532	BL00528	Ribosomal protein S4e proteins.	BL00528D 27.17 8.012e-09 341-395

SEQ ID NO:	Accession No.	Description	Results*
534	PR00194	TROPOMYOSIN SIGNATURE	PR00194C 6.38 1.900e-35 109-138 PR00194E 8.74 1.000e-30 195-221 PR00194D 9.57 8.714e-27 139-163 PR00194B 10.24 2.800e-25 84-105 PR00194A 7.86 5.500e-22 48-66
535	PR00194	TROPOMYOSIN SIGNATURE	PR00194C 6.38 1.900e-35 109-138 PR00194E 8.74 1.000e-30 195-221 PR00194B 10.24 2.800e-25 84-105 PR00194D 9.57 1.900e-23 139-163 PR00194A 7.86 5.500e-22 48-66
538	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 5.050e-11 110-124
541	BL00540	Ferritin iron-binding regions proteins.	BL00540A 15.06 1.000e-40 32-73 BL00540B 18.82 1.000e-40 123-178 BL00540C 13.00 7.750e-14 188-200
546	PR00153	CYCLOPHILIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153E 9.10 2.385e-15 121-137
548	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 8.213e-09 63-112
549	BL01282	BIR repeat proteins.	BL01282B 30.49 2.373e-12 317-356
551	BL00570	Bacterial ring hydroxylating dioxygenases alpha-subunit signa.	BL00570B 19.03 9.357e-09 277-309
553	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 7.000e-11 127-168
554	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.632e-11 447-461
555	PD02637	SERUM PARAOXONASE/ARYLES TERASE P.	PD02637A 14.26 1.000e-40 32-87 PD02637G 13.82 1.000e-40 307-355 PD02637D 13.69 6.053e-36 170-218 PD02637B 10.33 8.875e-34 106-141 PD02637E 11.92 8.200e-28 218-249 PD02637C 7.53 3.520e-27 141-170 PD02637F 15.62 9.438e-26 281-307
556	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 2.768e-16 474-508
557	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 5.179e-36 294-340 BL00039A 18.44 7.955e-29 15-54 BL00039C 15.63 1.300e-16 143-167 BL00039B 19.19 2.465e-12 58-84
558	PR00507	N12 CLASS N6 ADENINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00507B 14.16 8.932e-09 83-98
559	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 8.683e-12 242-253
566	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.500e-13 214-227
572	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 4.432e-09 76-130
573	BL00422	Granins proteins.	BL00422C 16.18 4.638e-10 49-77
574	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319A 15.27 7.911e-10 452-469 PR00319A 15.27 2.180e-09 410-427
577	BL00269	Mammalian defensins proteins.	BL00269C 16.52 6.786e-26 73-102 BL00269A 8.53 2.607e-20 8-28 BL00269B

SEQ ID NO:	Accession No.	Description	Results*
			19.17 5.500e-17 35-64
578	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327B 19.84 2.241e-11 157-179
579	BL00596	High potential iron-sulfur proteins.	BL00596B 13.07 9.743e-09 273-285
580	BL00915	Phosphatidylinositol 3- and 4-kinases proteins.	BL00915C 22.43 8.147e-32 1015-1054 BL00915D 27.02 9.217e-27 1092-1128 BL00915B 22.78 3.382e-25 918-956 BL00915A 10.09 5.500e-10 756-768
584	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 7.488e-09 499-520
585	BL00795	Involucrin proteins.	BL00795C 17.06 9.200e-09 498-543
586	BL00710	Phosphoglucomutase and phosphomannomutase phosphoserine signa.	BL00710 12.98 9.100e-17 159-174
587	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.714e-10 34-43
588	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.979e-14 257-278
591	BL00548	Ribosomal protein S3 proteins.	BL00548 20.58 7.000e-19 66-96
592	BL00478	LIM domain proteins.	BL00478B 14.79 1.250e-12 557-572 BL00478B 14.79 6.000e-12 494-509 BL00478B 14.79 2.400e-11 624-639
594	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 3.681e-13 141-160
596	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.063e-12 510-525 PR00049D 0.00 8.286e-10 513-528 PR00049D 0.00 9.000e-10 509-524 PR00049D 0.00 9.429e-10 511-526
599	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 4.750e-40 142-190 BL00232A 27.72 3.793e-22 48-81 BL00232B 32.79 1.257e-16 251-299 BL00232C 10.65 5.935e-14 249-267 BL00232D 16.25 3.368e-13 763-778 BL00232B 32.79 3.512e-11 366-414
600	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 9.695e-09 513-546
601	PF00583	Acetyltransferase (GNAT) family.	PF00583B 10.18 9.100e-10 120-130
602	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.950e-11 146-167
604	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 6.000e-10 136-170
607	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 4.717e-25 477-522 BL00239E 17.14 5.897e-23 423-473 BL00239C 18.75 7.600e-17 372-395
608	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.357e-32 10-49
609	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 4.808e-10 5-27 PR00449D 10.79 5.636e-09 111-125
610	PF00791	Domain present in ZO-1 and	PF00791C 20.98 2.412e-09 1-40

SEQ ID NO:	Accession No.	Description	Results*
		Unc5-like netrin receptors.	
612	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 9.234e-13 487-506
613	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.600e-10 104-115 BL00678 9.67 5.737e-09 62-73 BL00678 9.67 8.105e-09 146-157 BL00678 9.67 8.105e-09 276-287
615	PR00334	HMW KININOGEN SIGNATURE	PR00334B 8.69 5.230e-10 460-484 PR00334B 8.69 1.771e-09 464-488 PR00334B 8.69 2.886e-09 466-490 PR00334B 8.69 8.200e-09 458-482
617	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 5.881e-09 66-99
618	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 7.188e-10 539-551 PF00084B 9.45 7.300e-09 600-612
619	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 4.316e-09 72-92
621	BL00845	CAP-Gly domain proteins.	BL00845 16.43 1.900e-25 321-346 BL00845 16.43 9.325e-22 443-468
622	BL01002	Translationally controlled tumor protein.	BL01002D 18.24 4.706e-26 143-171 BL01002C 21.97 6.143e-26 79-110 BL01002A 13.19 1.360e-24 1-24 BL01002B 7.39 3.118e-14 48-62
624	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.857e-10 1030-1045
627	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011A 14.06 4.822e-09 475-494
629	PF00930	Dipeptidyl peptidase IV (DPP IV) N-terminal region.	PF00930I 15.96 5.000e-15 656-684 PF00930J 8.78 6.045e-12 708-729
630	PF00930	Dipeptidyl peptidase IV (DPP IV) N-terminal region.	PF00930I 15.96 5.000e-15 598-626 PF00930J 8.78 6.045e-12 650-671
631	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 1.844e-10 365-402
632	BL00114	Phosphoribosyl pyrophosphate synthetase proteins.	BL00114A 17.22 1.000e-40 54-101 BL00114B 15.90 1.000e-40 107-153 BL00114D 21.45 1.000e-40 208-259 BL00114C 18.22 2.895e-34 167-202 BL00114E 14.48 3.647e-25 293-317
635	BL00870	Chaperonins clpA/B proteins.	BL00870F 8.73 4.833e-36 376-425 BL00870G 8.07 6.553e-27 436-470 BL00870E 17.62 3.333e-16 304-359
639	BL00633	Bromodomain proteins.	BL00633B 13.82 9.775e-13 237-262 BL00633B 13.82 4.750e-11 80-105
641	BL00299	Ubiquitin domain proteins.	BL00299 28.84 7.962e-17 47-99
642	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 4.176e-10 97-141
643	PD02080	T-CELL GLYCOPROTEIN CD8 CHAIN SURFACE ALPHA PRE.	PD02080D 15.22 6.557e-09 269-306
644	BL01245	RIO1/ZK632.3/MJ0444 family proteins.	BL01245F 18.75 7.805e-14 239-276
646	BL00469	Nucleoside diphosphate kinases proteins.	BL00469 22.22 1.000e-40 41-96
649	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 5.945e-09 91-107
651	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 7.600e-11 629-650

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652	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 8.322e-09 227-260
653	PF01298	Transferrin binding protein.	PF01298C 15.13 1.000e-08 413-440
658	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE	PR00443A 15.16 9.451e-09 89-105
659	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.714e-10 34-43
663	BL00466	TFIIS zinc ribbon domain proteins.	BL00466 25.88 1.000e-32 294-331
664	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 3.172e-10 411-425
665	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.882e-11 10-29
669	PR00124	ATP SYNTHASE C SUBUNIT SIGNATURE	PR00124A 8.81 8.347e-11 117-137
670	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.	PD01234B 15.53 2.500e-10 38-56
671	BL00466	TFIIS zinc ribbon domain proteins.	BL00466 25.88 1.000e-32 219-256
672	BL01282	BIR repeat proteins.	BL01282B 30.49 2.068e-12 298-337
673	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 4.176e-14 201-217
674	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 8.703e-10 407-461 BL01160B 19.54 2.373e-09 414-468
675	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.286e-10 326-335
676	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.286e-10 335-344
682	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 4.789e-09 499-518
691	BL00415	Synapsins proteins.	BL00415Q 2.23 2.885e-09 83-119
692	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 6.167e-09 115-136
694	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 7.300e-09 297-312
696	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	PD02952C 15.76 5.701e-16 263-293 PD02952B 15.57 7.242e-11 243-257 PD02952A 11.84 9.625e-09 131-159
697	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e-15 504-517 PD00066 13.92 5.800e-14 220-233 PD00066 13.92 1.000e-11 248-261 PD00066 13.92 5.696e-11 333-346 PD00066 13.92 2.500e-09 361-374
698	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 6.571e-13 167-185
699	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 4.966e-09 50-65 PR00049D 0.00 9.237e-09 74-89
701	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 6.600e-15 98-116 PR00988C 13.64 5.605e-13 175-191 PR00988E 8.27 8.393e-13 245-257 PR00988D 5.95 8.250e-11 231-242 PR00988F 12.23 9.820e-11 267-281 PR00988B 11.60 2.317e-10 128-140
702	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625A 12.84 1.804e-13 22-42 PR00625B 13.48 5.821e-13 53-74
706	PF00023	Ank repeat proteins.	PF00023A 16.03 2.286e-09 209-225
708	BL01212	ATP P2X receptors proteins.	BL01212A 34.89 1.000e-40 43-96 BL01212E 24.87 1.000e-40 227-282 BL01212D 11.42 6.700e-25 185-209 BL01212G 11.86 2.800e-24 310-338 BL01212B 19.25 3.571e-21 129-154

SEQ ID NO:	Accession No.	Description	Results*
			BL01212C 8.40 1.214e-14 162-173 BL01212F 10.12 4.774e-14 291-302
709	BL00194	Thioredoxin family proteins.	BL00194 12.16 3.455e-17 45-58
712	BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	BL00439F 26.22 1.000e-40 418-471 BL00439E 19.05 2.440e-24 320-349 BL00439B 16.82 1.000e-20 167-189 BL00439H 18.24 4.600e-20 566-592 BL00439A 9.40 1.237e-15 35-52 BL00439D 13.11 4.545e-15 272-290 BL00439C 13.53 1.730e-11 248-261 BL00439G 13.40 9.719e-11 513-524
716	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.990e-09 305-356
718	BL01271	Sodium:sulfate symporter family proteins.	BL01271D 25.26 5.979e-32 537-592 BL01271A 8.06 6.250e-18 131-151 BL01271C 13.62 7.750e-17 464-486 BL01271B 12.02 1.563e-16 269-294
719	PF00023	Ank repeat proteins.	PF00023B 14.20 2.500e-10 141-151 PF00023A 16.03 4.000e-10 112-128
721	PF00023	Ank repeat proteins.	PF00023A 16.03 1.750e-10 66-82 PF00023B 14.20 5.500e-09 161-171 PF00023A 16.03 8.714e-09 363-379
725	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.500e-11 173-187 PR00019A 11.19 2.800e-11 314-328 PR00019A 11.19 5.050e-11 176-190 PR00019B 11.36 3.520e-09 311-325 PR00019B 11.36 4.600e-09 541-555 PR00019B 11.36 5.320e-09 471-485 PR00019A 11.19 6.000e-09 544-558 PR00019B 11.36 8.200e-09 242-256 PR00019B 11.36 9.640e-09 127-141
731	PR00681	RIBOSOMAL PROTEIN S1 SIGNATURE	PR00681I 8.81 9.897e-09 600-619
736	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.581e-31 8-47
739	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 1.587e-13 170-188 BL00972D 22.55 8.826e-11 590-615
740	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 1.587e-13 170-188 BL00972D 22.55 8.826e-11 590-615
741	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 6.936e-10 85-117
747	PF00646	F-box domain proteins.	PF00646A 14.37 6.625e-09 50-64
753	BL01168	Ribosomal protein S27e proteins.	BL01168 15.74 1.000e-40 20-75
756	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.885e-10 127-140
757	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 7.231e-09 1019-1030
761	BL00712	Ribosomal protein S17e proteins.	BL00712B 12.56 1.000e-40 28-66 BL00712A 6.23 8.855e-19 2-22
762	PF00878	Cation-independent mannose-6-phosphate receptor repeat proteins.	PF00878T 17.51 3.818e-09 799-826
763	BL00303	S-100/ICaBP type calcium binding protein.	BL00303A 21.77 9.526e-31 3-40 BL00303B 26.15 5.737e-30 50-87
766	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 6.087e-09 237-250
768	BL00221	MIP family proteins.	BL00221D 12.33 6.143e-19 180-195 BL00221C 13.36 1.000e-14 135-152 BL00221E 8.47 3.739e-13 203-214

SEQ ID NO:	Accession No.	Description	Results*
			BL00221B 10.22 1.750e-12 63-74 BL00221A 6.39 5.200e-12 16-27
769	PF00992	Troponin.	PF00992A 16.67 8.859e-10 214-249
770	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 8.297e-15 136-160
771	PR00883	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN SIGNATURE	PR00883A 6.49 8.920e-09 191-205
772	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 6.786e-32 8-47
775	BL00301	GTP-binding elongation factors proteins.	BL00301B 20.09 5.500e-31 90-122 BL00301C 11.73 8.200e-15 423-437 BL00301A 12.41 3.842e-13 9-21
776	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE	PR00453A 12.79 4.892e-12 325-343 PR00453B 14.65 1.614e-10 162-177 PR00453A 12.79 3.152e-10 123-141
779	PR00399	SYNAPTOTAGMIN SIGNATURE	PR00399A 9.52 1.730e-13 145-161 PR00399B 14.27 2.059e-13 160-174 PR00399C 12.82 7.324e-12 216-232 PR00399D 14.48 3.930e-10 236-247 PR00399B 14.27 1.915e-09 291-305
780	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 8.395e-10 123-172 BL00115Z 3.12 4.375e-09 137-186
783	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.800e-14 165-178 PD00066 13.92 8.800e-14 193-206 PD00066 13.92 5.286e-12 249-262 PD00066 13.92 8.269e-10 221-234
786	PF00975	Thioesterase domain proteins.	PF00975B 10.82 2.688e-12 90-104
788	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 9.833e-16 632-645
789	BL00740	MAM domain proteins.	BL00740B 19.76 5.378e-12 174-195 BL00740C 15.93 4.000e-11 684-695
793	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYN.	PD00289 9.97 9.500e-12 102-116
795	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038A 13.61 3.400e-09 66-82
800	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.050e-15 233-272
804	BL00663	Vinculin family talin-binding region proteins.	BL00663G 24.17 1.000e-40 364-414 BL00663K 21.52 9.816e-40 735-790 BL00663I 27.27 4.447e-35 514-568 BL00663J 18.16 3.000e-33 690-727 BL00663L 20.67 9.118e-27 802-838 BL00663F 20.78 2.000e-25 292-333 BL00663H 27.09 1.703e-24 436-489 BL00663C 22.59 2.853e-23 104-159 BL00663B 27.86 4.629e-23 42-96 BL00663D 24.77 3.789e-18 179-226 BL00663A 11.51 2.350e-15 18-39 BL00663E 21.19 9.566e-10 227-265
808	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 7.545e-10 3968-3979
809	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 7.545e-10 3882-3893

SEQ ID NO:	Accession No.	Description	Results*
810	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.929e-10 163-196
811	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 9.182e-15 243-261 PR00205A 14.73 1.000e-12 168-184 PR00205C 13.65 1.783e-12 503-518 PR00205B 11.39 9.294e-11 463-481
813	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.146e-11 313-328 PR00456E 3.06 5.146e-11 314-329 PR00456E 3.06 5.146e-11 315-330 PR00456E 3.06 7.938e-10 312-327 PR00456E 3.06 7.938e-10 316-331
818	BL01071	grpE protein.	BL01071A 24.88 8.277e-21 78-124 BL01071B 18.21 5.286e-15 195-219
826	DM00813	AMINOTRANSFERASES CLASS-V PYRIDOXAL-PHOSPHATE ATTACHMENT SI.	DM00813A 20.30 8.898e-17 231-260
828	BL00415	Synapsins proteins.	BL00415P 2.37 9.814e-09 242-278
830	PF00632	HECT-domain (ubiquitin-transferase).	PF00632C 20.66 5.186e-23 1534-1566 PF00632B 18.45 8.393e-22 1480-1508
831	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 9.695e-09 117-150
832	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.231e-33 12-51
834	BL00120	Lipases, serine proteins.	BL00120B 11.37 5.846e-09 1319-1334
836	DM00813	AMINOTRANSFERASES CLASS-V PYRIDOXAL-PHOSPHATE ATTACHMENT SI.	DM00813A 20.30 8.898e-17 38-67
838	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYN.	PD00289 9.97 8.000e-12 69-83
840	BL00053	Ribosomal protein S8 proteins.	BL00053B 14.56 1.000e-08 900-918
841	PR00970	ARGININE ADP-RIBOSYLTRANSFERASE SIGNATURE	PR00970D 9.96 3.357e-17 129-146 PR00970A 17.73 8.600e-17 30-52 PR00970E 11.23 6.464e-15 177-193 PR00970B 16.37 2.756e-11 58-77 PR00970C 11.05 9.357e-11 89-104
842	BL00250	TGF-beta family proteins.	BL00250A 21.24 7.120e-25 114-150 BL00250B 27.37 4.774e-18 178-214
846	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.488e-10 156-180
848	BL01095	Chitinases family 18 proteins.	BL01095B 10.82 5.500e-14 24-36 BL01095C 10.76 7.207e-10 246-258
849	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e-34 300-343
850	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00318A 7.84 7.088e-09 188-204
851	PF00969	Class II histocompatibility antigen, beta domain proteins.	PF00969A 22.07 5.846e-29 12-55 PF00969B 9.97 6.211e-25 56-92 PF00969C 27.72 7.324e-16 95-145
852	BL00269	Mammalian defensins proteins.	BL00269B 19.17 6.824e-21 34-63 BL00269A 8.53 6.108e-18 1-21
853	PF00777	Sialyltransferase family.	PF00777B 29.69 8.767e-10 407-450
856	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191D 13.94 9.083e-10 100-139

SEQ ID NO:	Accession No.	Description	Results*
857	PR00823	PANCREATIC LIPASE SIGNATURE	PR00823A 18.01 3.143e-14 19-37 PR00823C 6.88 6.164e-12 56-69
859	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.684e-09 243-254
860	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 8.650e-13 425-442 BL00028 16.07 5.696e-12 508-525 BL00028 16.07 8.826e-12 564-581 BL00028 16.07 7.577e-11 201-218 BL00028 16.07 7.577e-11 536-553 BL00028 16.07 7.923e-11 341-358 BL00028 16.07 8.615e-11 285-302 BL00028 16.07 1.600e-10 592-609 BL00028 16.07 2.200e-10 229-246 BL00028 16.07 3.400e-10 257-274 BL00028 16.07 6.100e-10 313-330 BL00028 16.07 7.000e-10 369-386 BL00028 16.07 8.200e-10 397-414 BL00028 16.07 5.114e-09 620-637
864	BL01126	Elongation factor Ts proteins.	BL01126A 18.48 5.011e-10 2637-2680
865	BL00353	HMG1/2 proteins.	BL00353B 11.47 1.330e-13 95-145 BL00353B 11.47 5.692e-11 353-403
866	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 4.600e-18 173-191 BL00972D 22.55 1.947e-13 576-601 BL00972E 20.72 2.038e-11 618-640
867	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 2.756e-12 255-266
872	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 5.737e-09 69-79
873	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 4.405e-19 50-87 BL00303A 21.77 8.765e-15 3-40
874	BL00523	Sulfatases proteins.	BL00523A 13.36 6.500e-17 41-58 BL00523B 8.64 5.909e-15 89-101 BL00523C 12.64 5.500e-13 140-151 BL00523D 9.89 9.438e-11 293-305
877	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.000e-40 42-90
881	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.727e-11 116-128 PR00081A 10.53 3.106e-10 40-58
882	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.391e-39 50-98
883	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.391e-39 50-98
888	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.929e-30 232-275

Results include Accession number, sub type, eMatrix p-value and the position of the signature.

TABLE 4

SEQ ID NO:	Pfam Model	Description	E-value	Pfam Score
445	Rap_GAP	Rap/ran-GAP	6.2e-121	415.2
446	zf-C2H2	Zinc finger, C2H2 type	7.4e-65	228.9
452	WD40	WD domain, G-beta repeat	0.00017	28.4
465	WD40	WD domain, G-beta repeat	1.3e-19	78.6
483	COesterase	Carboxylesterases	2.1e-128	440.0
484	hexokinase	Hexokinase	0	2009.4
485	zf-C2H2	Zinc finger, C2H2 type	1e-135	464.2
486	GTP_EFTU	Elongation factor Tu family	3.2e-125	424.7
487	myosin_head	Myosin head (motor domain)	1.5e-283	955.3
488	Glyco_transf_8	Glycosyl transferase family 8	4e-12	53.7
489	tubulin	Tubulin/PtsZ family	3.2e-293	987.5
492	pkinase	Eukaryotic protein kinase domain	7.9e-85	295.2
493	SH3	SH3 domain	1.2e-18	75.4
497	Syntaxin	Syntaxin	0.074	-75.1
498	SCAN	SCAN domain	5.4e-67	236.0
499	F-box	F-box domain	0.0002	28.1
501	FHA	FHA domain	1.7e-13	58.3
502	Collagen	Collagen triple helix repeat (20 copies)	6.5e-197	667.6
507	PH	PH domain	3e-15	59.5
508	CH	Calponin homology (CH) domain	0.0069	16.3
512	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	5.7e-31	116.3
516	DnaJ	DnaJ domain	1.4e-24	95.1
519	DnaJ	DnaJ domain	6.8e-26	99.5
522	Glycos_transf_2	Glycosyl transferases	1.2e-13	58.8
523	globin	Globin	4.1e-38	137.3
526	myosin_head	Myosin head (motor domain)	0	1057.8
529	Acetyltransf	Acetyltransferase (GNAT) family	5e-11	50.1
530	MSP_domain	MSP (Major sperm protein) domain	1.7e-16	68.2
531	7tm_2	7 transmembrane receptor (Secretin family)	1.3e-59	211.5
534	Tropomyosin	Tropomyosin	7e-177	553.3
535	Tropomyosin	Tropomyosin	3.1e-173	541.9
538	LRR	Leucine Rich Repeat	2.9e-23	90.7
539	tRNA-synt_1b	tRNA synthetases class I (W and Y)	7.9e-79	275.3
540	PAS	PAS domain	2.8e-05	24.9
541	ferritin	Ferritin	9.9e-116	391.6
546	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	3.5e-33	117.6
549	KH-domain	KH domain	0.0004	27.1
551	Glyco_transf_8	Glycosyl transferase family 8	0.01	-47.7
554	zf-C2H2	Zinc finger, C2H2 type	2.6e-22	87.5
555	Arylesterase	Arylesterase	2.3e-211	715.6
556	G-patch	G-patch domain	2.4e-17	71.1
557	DEAD	DEAD/DEAH box helicase	8.7e-67	214.2
558	Methyltransf_4	Putative methyltransferase	0.0095	-48.4
559	DSPc	Dual specificity phosphatase, catalytic dom	4.8e-70	246.1
563	IPPT	IPP transferase	6.7e-66	232.4
566	zf-C2H2	Zinc finger, C2H2 type	2.6e-19	77.6
570	RNA_pol_L	RNA polymerases L / 13 to 16 kDa subunit	0.043	-12.1
571	Armadillo_seg	Armadillo/beta-catenin-like repeat	8.6e-33	122.4
574	WD40	WD domain, G-beta repeat	1.1e-65	231.6
576	PAP2	PAP2 superfamily	1.2e-19	78.7
577	Defensin_propep	Defensin propeptide	3e-25	97.3
578	ig	Immunoglobulin domain	3.5e-16	57.2
580	PI3_PI4_kinase	Phosphatidylinositol 3- and 4-kinase	6.5e-93	322.1

SEQ ID NO:	Pfam Model	Description	E-value	Pfam Score
585	GBP	Guanylate-binding protein, N-terminal domain	4.3e-165	548.2
586	PGM_PMM_I	Phosphoglucosyltransferase/phosphomannomutase, alp	7.6e-06	4.4
587	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.3e-11	41.9
588	MMR_HSR1	GTPase of unknown function	5.9e-48	172.7
590	zf-DHHC	DHHC zinc finger domain	1.8e-36	134.6
591	Ribosomal_S3_C	Ribosomal protein S3, C-terminal domain	1.3e-07	28.0
592	LIM	LIM domain	4.4e-27	103.4
594	pkinase	Protein kinase domain	3.7e-77	269.7
596	PX	PX domain	2.2e-17	71.2
599	Cadherin_C_term	Cadherin cytoplasmic region	3.3e-88	306.5
600	FHA	FHA domain	3.4e-20	80.5
601	Acetyltransf	Acetyltransferase (GNAT) family	3.2e-17	70.6
604	NAP_family	Nucleosome assembly protein (NAP)	5.5e-12	46.4
605	RhoGAP	RhoGAP domain	1e-28	108.9
606	Armadillo_seg	Armadillo/beta-catenin-like repeat	0.00022	28.0
607	pkinase	Protein kinase domain	5.9e-77	269.1
608	zf-C2H2	Zinc finger, C2H2 type	5.4e-110	378.8
609	ras	Ras family	1.2e-16	52.8
610	ank	Ank repeat	1.6e-08	41.8
612	pkinase	Protein kinase domain	1.6e-69	244.3
613	WD40	WD domain, G-beta repeat	4.7e-55	196.3
614	UBA	UBA/TS-N domain	3.6e-12	53.9
615	Zip	ZIP Zinc transporter	8.1e-59	208.8
618	sushi	Sushi domain (SCR repeat)	1.3e-58	208.2
619	K_tetra	K ⁺ channel tetramerisation domain	1.3e-19	78.6
621	CAP_GLY	CAP-Gly domain	1.9e-48	174.3
622	TCTP	Translationally controlled tumor protein	5.2e-109	375.5
628	UQ_con	Ubiquitin-conjugating enzyme	0.0046	-43.3
629	DPPIV_N_term	Dipeptidyl peptidase IV (DPP IV) N-termi	5.1e-07	-82.1
630	DPPIV_N_term	Dipeptidyl peptidase IV (DPP IV) N-termi	5.5e-07	-83.2
631	efhand	EF hand	2.3e-14	61.1
632	Pribosyltran	Phosphoribosyl transferase domain	4.3e-37	136.7
635	ank	Ank repeat	1.8e-25	98.0
636	MHCK_EF2_kinase	MHCK/EF2 kinase domain family	1.2e-12	5.6
637	DUF221	Domain of unknown function DUF221	1.2e-89	311.2
639	bromodomain	Bromodomain	2.2e-29	106.0
641	ubiquitin	Ubiquitin family	2.2e-21	81.9
644	RJO1	RJO1/ZK632.3/MJ0444 family	1.1e-07	-14.9
646	NDK	Nucleoside diphosphate kinase	1.1e-52	188.4
649	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	9.4e-12	42.4
651	ABC_tran	ABC transporter	7.9e-84	291.9
654	CUB	CUB domain	3e-30	113.9
655	MHCK_EF2_kinase	MHCK/EF2 kinase domain family	2.6e-09	-35.3
659	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.3e-11	41.9
661	UvrD-helicase	UvrD/REP helicase	0.078	9.7
663	TFIIS	Transcription factor S-II (TFIIS)	2e-22	87.9
664	dsrm	Double-stranded RNA binding motif	4.3e-42	153.3
665	rrm	RNA recognition motif	0.002	24.8
669	OTU	OTU-like cysteine protease	1e-19	78.9
671	TFIIS	Transcription factor S-II (TFIIS)	2e-22	87.9
672	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.5e-05	22.3
673	AMP-binding	AMP-binding enzyme	1.6e-86	300.9

SEQ ID NO:	Pfam Model	Description	E-value	Pfam Score
679	MSP domain	MSP (Major sperm protein) domain	5.4e-18	73.2
680	MSP domain	MSP (Major sperm protein) domain	5.5e-11	49.9
683	RNase PH	3' exoribonuclease family	3e-42	153.8
684	lactamase_B	Metallo-beta-lactamase superfamily	0.088	-15.6
686	tRNA anti	OB-fold nucleic acid binding domain	0.031	20.9
690	NHL	NHL repeat	8.2e-18	72.6
691	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	6.1e-09	33.2
693	WD40	WD domain, G-beta repeat	0.025	21.2
694	WD40	WD domain, G-beta repeat	1.1e-23	92.1
696	Choline kinase	Choline/ethanolamine kinase	1.6e-51	184.6
697	zf-C2H2	Zinc finger, C2H2 type	3.4e-74	259.9
698	cadherin	Cadherin domain	2.2e-05	31.3
701	PRK	Phosphoribulokinase / Uridine kinase family	1.1e-79	278.1
702	DnaJ	DnaJ domain	5e-26	99.9
888	PAX	'Paired box' domain	1.1e-87	304.7

TABLE 5

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
445	1b8q	A	324	401	1.30E-07	0.39	0.99		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B; PSD-95; CHAIN: A; CRPT; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
445	1be9	A	355	401	0.00014	-0.32	0.65		INTERLEUKIN 16; CHAIN: NULL;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
445	1i16		329	414	1.30E-05	0.58	0.48		HCASK/LIN-2 PROTEIN; CHAIN: A; B;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
445	1kwa	A	329	404	1.10E-11	0.26	0.8		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
445	1qau	A	325	410	7.00E-11	0.7	1		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	OXIDOREDUCTASE BETA-FINGER
445	1qav	A	324	396	5.60E-10	0.2	0.81		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
445	3pdz	A	324	414	2.80E-05	0.64	0.74		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTPIE, PTP-BAS, SPECIFICITY 2 OF BINDING
446	1alh	A	109	189	1.70E-30	0.24	1		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
446	1alh	A	137	248	1.70E-23	-0.03	0.11		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
446	1alh	A	194	278	4.20E-29			80.51	QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
446	1alh	A	195	277	4.20E-29	0.16	1		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	FINGER, DNA-BINDING PROTEIN
446	1alh	A	205	276	6.80E-28	-0.05	1		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
446	1alh	A	224	303	8.50E-28	-0.09	1		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
446	1alh	A	252	331	1.50E-28	-0.18	0.99		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
446	1alh	A	280	359	1.20E-30	-0.24	1		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
446	1alh	A	53	133	5.10E-20	0.1	0.05		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
446	1alh	A	81	189	4.20E-25	-0.35	0.21		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
446	1mey	C	108	189	1.20E-49	0.35	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1mey	C	136	220	1.70E-38	0.38	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1mey	C	164	276	1.00E-44	0.11	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
446	1mey	C	223	303	1.70E-47	0.15	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1mey	C	27	105	5.10E-21	0.08	-0.13		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1mey	C	278	360	1.00E-48			97.55	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1mey	C	279	360	1.00E-48	0.11	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1mey	C	53	133	5.10E-37	0.19	0.75		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1mey	C	80	161	1.00E-48	0.53	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1mey	C	83	190	4.20E-27	-0.13	0.36		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1mey	G	78	105	5.10E-12	0.39	0.19		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
446	1tf3	A	108	192	1.20E-20			62.34	TRANSCRIPTION FACTOR	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
446	1tf3	A	109	189	1.20E-20	0.22	0.53		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
446	1tf3	A	60	129	1.00E-14	-0.07	0.05		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
446	1tf6	A	108	281	1.70E-36			124.38	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
446	1tf6	A	109	257	1.70E-36	0.37	0.94		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
446	1tf6	A	204	347	1.40E-35	-0.14	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
446	1tf6	A	60	189	3.40E-30	0.11	0.86		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
446	1t66	A	81	229	8.50E-32	-0.04	0.87		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
446	1ubd	C	106	248	2.80E-32	-0.12	0.92		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	116	220	1.70E-28	0.01	0.96		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	144	276	1.50E-30	0.01	0.72		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	169	276	2.80E-35	0.09	1		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	198	331	9.80E-36	-0.01	0.98		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
446	1ubd	C	205	303	5.10E-32	0.08	0.93		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	221	359	2.80E-31	-0.08	1		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	253	360	9.80E-36			105.01	YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	256	359	3.40E-34	0.01	1		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	27	133	5.10E-23	0.24	0.11		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	53	161	5.10E-30	0.37	1		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	1ubd	C	85	189	1.40E-32	0.11	0.99		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
446	2adr		53	107	1.70E-09	0.04	-0.19		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
446	2gli	A	109	331	2.80E-42	0.05	0.21		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
446	2gli	A	116	275	5.10E-29	0.04	0.11		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
446	2gli	A	165	359	1.10E-41	0.11	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
446	2gli	A	195	333	2.80E-42			99.39	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
446	2gli	A	207	330	3.40E-30	0.46	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
446	2gli	A	231	358	3.40E-32	0.27	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
446	2gli	A	32	160	3.40E-27	0.48	0.4		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
446	2gli	A	83	278	2.80E-45	-0.1	0.93		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	BINDING PROTEIN/DNA COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
446	2gli	A	88	247	8.50E-31	0.31	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
447	1aj3		39	139	6.80E-16	0.28	0.09		ALPHA SPECTRIN; CHAIN: NULL;	CYTOSKELETON ELASTICITY, MEMBRANE SKELETON, SPECTRIN, COILED-COIL, 2 CYTOSKELETON, CALMODULIN-BINDING, ACTIN-BINDING, 3 CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 4 SH3 DOMAIN
447	1cun	A	2	142	1.00E-17	-0.21	0.23		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
447	1cun	A	3	201	5.60E-05	-0.17	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
447	1cun	A	37	262	1.70E-23			57.3	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
447	1cun	A	38	259	1.70E-23	-0.07	0.33		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
447	1fio	A	10	121	0.00028	-0.32	0.29		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
447	1quu	A	23	267	1.70E-19			64.46	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN:	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
447	1quu	A	256	322	0.0012	-0.31	0.16		A; HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	PROTEIN CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
447	1quu	A	27	265	1.70E-19	-0.19	0.11		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
450	1elr	A	110	190	5.10E-05	-0.26	0.27		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
450	1elr	A	128	220	0.0014	-0.49	0		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
450	1elw	A	71	186	1.20E-08	0.41	0.3		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
450	1fch	A	128	278	0.0084	-0.37	0.16		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
450	1fch	A	289	580	4.20E-07	0.12	0.49		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
452	1ejj	A	4	213	5.10E-38	0.01	0.19		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
458	1af7		2	146	0.0098	-0.22	0.29		CHEMOTAXIS RECEPTOR METHYLTRANSFERASE CHER; CHAIN: NULL;	METHYLTRANSFERASE METHYLTRANSFERASE, CHEMOTAXIS RECEPTOR METHYLATION
458	1xva	A	83	148	2.80E-06	-0.32	0.21		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B;	METHYLTRANSFERASE GNMT, S-ADENOSYL-L-METHIONINE; GLYCINE METHYLTRANSFERASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
459	1a7i		851	879	0.0042	-0.46	0.09		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
459	1b89	A	351	718	5.10E-33	0.11	0.16		CLATHRIN HEAVY CHAIN; CHAIN: A;	CLATHRIN CLATHRIN, TRISKELION, COATED VESICLES, ENDOCYTOSIS, SELF-2 ASSEMBLY, ALPHA-ALPHA SUPERHELIX
459	1cxx	A	851	879	0.0098	-0.39	0.04		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
465	1crz	A	225	481	0.0012	0.31	0.77		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
465	1crz	A	341	499	0.007	0.51	0.15		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
465	1erj	A	167	405	1.70E-48	0.31	0.28		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
465	1erj	A	181	500	5.10E-72	0.6	0.76		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
465	1erj	A	220	551	6.80E-63	0.31	0.15		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
465	1erj	A	282	599	8.50E-64	0.36	0.41		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
465	1erj	A	330	639	1.70E-61	-0.03	0.01		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
465	1got	B	129	499	1.40E-84			101.01	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
465	1got	B	165	499	1.40E-84	0.57	0.93		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
465	1got	B	326	639	8.50E-64	0.28	0.13		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
465	1qks	A	167	498	4.20E-36	0.2	0.37		CYTOCHROME C11 NITRITE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE ENZYME, NITRITE REDUCTASE, OXIDOREDUCTASE, DENITRIFICATION, 2 ELECTRON TRANSPORT, PERIPLASMIC
468	1fy7	A	17	290	0	0.6	1		ESA1 HISTONE ACETYLTRANSFERASE; CHAIN: A;	TRANSFERASE ESA1 HAT, ESA1 PROTEIN, ESA1P; HISTONE ACETYLTRANSFERASE, COENZYME A
470	1qhf	A	16	257	6.80E-75			238.98	PHOSPHOGLYCERATE MUTASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE (PHOSPHORYL)
470	1qhf	A	16	259	6.80E-75	0.89	1		PHOSPHOGLYCERATE MUTASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE (PHOSPHORYL)
470	3pg _m		16	249	7.00E-75	0.51	1		TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DEPHOSPHO ENZYME 3PGM 4	
470	3pg _m		16	250	7.00E-75			226.92	TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DEPHOSPHO ENZYME 3PGM 4	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
470	3pgm		16	251	1.50E-67	0.72	1		TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DEPHOSPHO ENZYME 3PGM 4	
473	1bor		27	70	3.40E-07	-0.13	0.04		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
473	1chc		28	73	5.60E-12	0.11	0.96		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
473	1chc		29	76	1.70E-11	-0.45	0.66		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
473	1fbv	A	27	71	8.40E-14	-0.26	0.51		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
473	1fbv	A	29	71	1.70E-11	-0.36	0.6		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
473	1g25	A	28	73	5.60E-13	-0.15	0.71		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
473	1g25	A	29	80	3.40E-06	0.21	0.43		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
473	1rmd		20	112	2.80E-25	-0.05	0.93		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
473	1rmd		23	114	5.10E-21	-0.26	0.86		RAG1; CHAIN: NULL;	CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
473	1rmd		7	114	2.80E-25			54.37	RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
473	1ubd	C	89	194	3.40E-11	-0.51	0.06		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
473	5znf		140	167	0.0042	-0.67	0.12		ZINC FINGER DNA BINDING DOMAIN ZINC-FINGER (ZFY-6T) (NMR, 13 STRUCTURES) 5ZNF 3	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
475	1avl	A	1	206	0.00056			61.09	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
475	1cun	A	13	219	0.00098			51.86	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
475	1hme		164	204	0.0014	-0.45	0.01		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
475	1hsm		164	210	0.00084	-0.39	0.12		(DNA-BINDING IHME 3 HMG-BOX DOMAIN B OF RAT HMG1) (NMR, 1 STRUCTURE) IHME 4	
475	1quu	A	1	222	4.20E-08			55.34	DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH IHSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) IHSM 4	
477	1bq0		108	182	1.20E-19			72.19	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
477	1bq0		110	181	1.20E-19	1.11	1		DNA1; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
477	1elr	A	6	129	1.20E-19	0.38	-0.09		DNA1; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
477	1elw	A	6	123	8.50E-24	0.42	0.05		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B; TPRI-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
477	1fch	A	7	108	1.00E-18	0	-0.02		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
477	1hdj		107	180	1.20E-19	1.05	1		HUMAN HSP40; CHAIN: NULL;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
477	1hdj		107	187	1.40E-30			80.39	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDI-1; MOLECULAR CHAPERONE
477	1hdj		109	176	1.40E-30	0.98	1		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDI-1; MOLECULAR CHAPERONE
479	1bif	A	43	76	0.00013	-0.35	0.39		NEUROCALCIN DELTA;	CALCIUM-BINDING CALCIUM-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
479	1c07	A	41	83	0.00014	-0.18	0.92		CHAIN: A, B; EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN
479	1c7w	A	41	83	0.00028	-0.3	0.42		CALCIUM VECTOR PROTEIN; CHAIN: A;	METAL BINDING PROTEIN CAVP; EF-HAND FAMILY, CALCIUM BINDING PROTEIN, NMR
479	1cdm	A	41	107	8.40E-05	0.54	0.51		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
479	1cll		41	103	4.20E-05	0.07	0.13		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
479	1cll	A	43	98	0.00017	0.28	0.12		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
479	1crr	A	41	103	0.00014	0.09	0.27		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
479	1fpw	A	43	84	5.60E-05	0.14	0.21		CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A;	METAL BINDING PROTEIN YEAST FREQUENIN EF-HAND, CALCIUM
479	1iku		42	96	0.00028	-0.43	0.05		RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
480	1buo	A	22	143	1.70E-24	0.11	0.63		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
480	1fqv	B	52	168	1.10E-05	-0.06	0.69		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
480	1fs1	B	52	141	4.20E-05	0.48	0.96		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
480	1fs2	B	52	164	0.00042	0.26	0.86		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE SKP2 F-BOX; SKP1; SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
480	1gof		318	577	1.40E-31	0.22	-0.08		OXIDOREDUCTASE(OXYGE N(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	LIGASE
480	1gof		346	588	8.50E-13	0.31	0.22		OXIDOREDUCTASE(OXYGE N(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	
480	1gof		362	592	2.80E-14	0.07	-0.18		OXIDOREDUCTASE(OXYGE N(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	
481	1bih	A	99	396	1.70E-29	0	-0.17		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
481	1cvs	D	303	396	1.40E-12	-0.04	0.21		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
481	1dgi	R	96	381	1.70E-14	0.03	-0.14		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
481	1ev2	E	303	392	5.10E-13	0.05	0.17		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, FGFR2, IMMUNOGLOBULIN (IG) LIKE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
481	1ev2	G	303	392	5.10E-13	-0.2	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
481	1ev1	C	303	396	1.40E-12	0.02	0.1		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
481	1f2q	A	192	386	1.70E-16	-0.2	0.04		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
481	1fhg	A	289	381	3.40E-17	0.13	-0.07		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN
481	1lko		292	382	8.50E-16	0.06	0.03		TWITCHIN; CHAIN: NULL;	IMMUNOGLOBULIN FOLD, BETA BARREL
481	2fcb	A	191	384	1.70E-14	-0.06	0.01		FC GAMMA RIIB; CHAIN: A;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
482	1elr	A	281	363	0.00014	-0.06	0.09		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
483	1a8s		152	296	0.0017	0.45	0.04		CHLOROPEROXIDASE F; CHAIN: NULL;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
483	1c4x	A	178	331	0.00012	0.29	0.47		2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE CHAIN: A; PARA-NITROBENZYL ESTERASE; CHAIN: A;	HALOPEROXIDASE HALOPEROXIDASE F; HALOPEROXIDASE, OXIDOREDUCTASE, PROPIONATE COMPLEX HYDROLASE BPHD; HYDROLASE, PCB DEGRADATION
483	1c7j	A	43	606	3.40E-93	0.39	1			HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE, DIRECTED

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
483	1cl	A	42	581	1.20E-73			181.19	CHOLESTEROL ESTERASE; ICLE 4 CHAIN: A, B; ICLE 5	EVOLUTION, ORGANIC ACTIVITY, 2 PNB ESTERASE LIPASE ESTERASE, SUBSTRATE/PRODUCT-BOUND ICLE 9
483	1cl	A	68	593	1.20E-73	0.21	1		CHOLESTEROL ESTERASE; ICLE 4 CHAIN: A, B; ICLE 5	LIPASE ESTERASE, SUBSTRATE/PRODUCT-BOUND ICLE 9
483	1cv2	A	163	379	0.0084	0.6	0.57		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXADIENE DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA-HYDROLASE
483	1dx4	A	40	611	0	0.61	1		ACETYLCHOLINESTERASE; CHAIN: A;	HYDROLASE (SERINE ESTERASE) HYDROLASE (SERINE ESTERASE), HYDROLASE, SERINE ESTERASE, 2 SYNAPSE, MEMBRANE, NERVE, MUSCLE, SIGNAL, NEUROTRANSMITTER 3 DEGRADATION, GLYCOPROTEIN, GPI-ANCHOR, ALTERNATIVE SPLICING
483	1ea5	A	40	612	0	0.59	1		ACETYLCHOLINESTERASE; CHAIN: A;	CHOLINESTERASE SERINE HYDROLASE, NEUROTRANSMITTER CLEAVAGE, CATALYTIC 2 TRIAD, ALPHA/BETA HYDROLASE
483	1evq	A	142	346	3.40E-28	0.17	0.58		SERINE HYDROLASE; CHAIN: A;	HYDROLASE ALPHA/BETA
483	1evq	A	73	283	5.60E-39	-0.05	0.42		SERINE HYDROLASE; CHAIN: A;	HYDROLASE FOLD HYDROLASE ALPHA/BETA HYDROLASE FOLD
483	1f6w	A	44	612	0	0.5	1		BILE SALT ACTIVATED LIPASE; CHAIN: A;	HYDROLASE BILE SALT ACTIVATED LIPASE, ESTERASE, CATALYTIC DOMAIN
483	1jkm	A	83	334	5.10E-20	-0.05	0.1		BREFELDIN A ESTERASE; CHAIN: A, B;	SERINE HYDROLASE SERINE HYDROLASE, DEGRADATION OF BREFELDIN A, ALPHA/BETA 2 HYDROLASE FAMILY
483	1lpp		42	581	1.20E-71			179.92	HYDROLASE LIPASE (E.C.3.1.1.3) (TRIACYLGLYCEROL LIPASE) COMPLEXED WITH	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									ILPP 3 HEXADECANESULFONATE ILPP 4 ILPP 71	
483	lpp		68	593	1.20E-71	0.22	1		HYDROLASE LIPASE (E.C.3.1.1.3) (TRIACYLGLYCEROL LIPASE) COMPLEXED WITH ILPP 3 HEXADECANESULFONATE ILPP 4 ILPP 71	
483	lmaa	A	38	612	0			368.25	ACETYLCHOLINESTERASE; CHAIN: A, B, C, D;	HYDROLASE MACHE; HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, TETRAMER, 2 HYDROLASE FOLD, GLYCOSYLATED PROTEIN
483	lmaa	A	38	612	0	0.72	1		ACETYLCHOLINESTERASE; CHAIN: A, B, C, D;	HYDROLASE MACHE; HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, TETRAMER, 2 HYDROLASE FOLD, GLYCOSYLATED PROTEIN
483	lqe3	A	40	602	1.70E-89			242.59	PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA- BETA HYDROLASE DIRECTED EVOLUTION
483	lqe3	A	43	599	1.70E-89	0.33	1		PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA- BETA HYDROLASE DIRECTED EVOLUTION
483	lqfm	A	26	397	5.60E-57	0.15	0.11		PROLYL OLIGOPEPTIDASE; CHAIN: A;	HYDROLASE PROLYL ENDOPEPTIDASE, POST-PROLINE CLEAVING PROLYL OLIGOPEPTIDASE, AMNESIA, ALPHA/BETA-HYDROLASE, BETA-2 PROPELLER
483	lqfm	A	87	350	1.20E-35	0	0.03		PROLYL OLIGOPEPTIDASE; CHAIN: A;	HYDROLASE PROLYL ENDOPEPTIDASE, POST-PROLINE CLEAVING PROLYL OLIGOPEPTIDASE, AMNESIA, ALPHA/BETA-HYDROLASE, BETA-2 PROPELLER
483	lthg		46	580	5.10E-80			210.1	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
483	1thg		47	583	5.10E-80	0.49	1		TRIACYLGLYCEROL HYDROLASE 1THG 3	
483	2bce		39	618	0			318.91	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) TRIACYLGLYCEROL HYDROLASE 1THG 3	
483	2bce		44	612	0	0.54	1		CHOLESTEROL ESTERASE; CHAIN: NULL;	HYDROLASE BILE SALT ACTIVATED LIPASE, BILE SALT STIMULATED HYDROLASE, SERINE ESTERASE, LIPASE
484	1bg3	A	1	910	0	1.19	1		HEXOKINASE; CHAIN: A, B;	HEXOKINASE ATP/D-HEXOSE-6-PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTRANSFERASE
484	1bg3	A	1	911	0			179.92	HEXOKINASE; CHAIN: A, B;	HEXOKINASE ATP/D-HEXOSE-6-PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTRANSFERASE
484	1cza	N	16	913	0	1.21	1		HEXOKINASE TYPE I; CHAIN: N;	PHOSPHOTRANSFERASE
485	1alh	A	127	204	1.70E-18	-0.49	0.11		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
485	1alh	A	152	232	1.70E-23	-0.36	0.3		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
485	1alh	A	180	260	6.80E-24	0.16	0.94		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
485	1me _y	C	126	204	1.70E-30	-0.34	0.11		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	151	232	5.10E-38	-0.18	0.69		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	179	260	8.50E-41	-0.01	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	207	288	1.20E-42	0.05	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	235	316	1.40E-43	0.27	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	291	372	2.80E-47	0.25	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	291	372	5.10E-47	0.25	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	319	400	1.50E-48	0.67	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	319	400	2.80E-51	0.67	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
485	1mey	C	347	428	5.10E-49	0.48	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	375	456	3.40E-49	0.69	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	375	456	4.20E-50	0.69	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	375	457	4.20E-50			113.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	403	484	1.00E-49	0.41	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	431	512	1.70E-50	0.05	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	459	540	1.50E-50	0.02	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1mey	C	487	568	8.50E-51	0.1	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
485	1me y	C	515	596	1.50E-50	0.02	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) ZINC COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1me y	C	543	624	3.40E-50	0.03	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1me y	C	571	652	1.70E-50	0.28	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1me y	C	599	680	3.40E-50	0.15	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1me y	C	627	683	1.00E-32	0.36	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1me y	G	149	176	5.10E-07	-0.38	0.48		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
485	1tf6	A	130	274	3.40E-27	-0.28	0.76		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE II, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
485	1tf6	A	152	297	3.40E-31	-0.2	0.81		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
485	1tf6	A	208	353	6.80E-34	0.07	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
485	1tf6	A	319	484	5.10E-37			120.46	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
485	1tf6	A	376	521	5.10E-37	0.11	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
485	1tf6	A	488	633	3.40E-37	0.01	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
485	1tf6	A	544	682	1.40E-36	0.1	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
485	1ubd	C	127	232	5.10E-25	-0.22	0.12		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	159	260	8.50E-27	-0.27	0.72		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	182	288	3.40E-29	-0.04	0.86		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	215	316	1.20E-29	0.32	0.93		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	238	344	8.50E-32	0.18	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	240	345	4.20E-46	0.02	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	268	372	7.00E-52	0.14	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	296	400	9.80E-59	0.63	1		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
485	1ubd	C	346	456	2.80E-59	0.04	1		ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	349	457	2.80E-59			100.22	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	401	512	2.80E-55	0.26	1		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	485	596	8.40E-56	0.1	1		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	1ubd	C	541	652	4.20E-59	0.09	1		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
485	1ubd	C	579	680	3.40E-34	0.06	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
485	2gli	A	131	262	1.00E-26	-0.05	0.09		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
485	2gli	A	179	346	5.60E-44	0.01	0.47		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
485	2gli	A	207	343	3.40E-31	0.4	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
485	2gli	A	263	402	1.40E-68	0.53	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
485	2gli	A	319	458	2.80E-77			110.36	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
485	2gli	A	319	458	2.80E-77	0.54	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
485	2gli	A	375	542	1.40E-73	0.01	0.88		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
485	2gli	A	487	654	1.10E-73	-0.12	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
485	2gli	A	516	681	1.40E-72	0.09	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
485	2gli	A	523	651	1.40E-34	0.23	0.94		D; ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
485	2gli	A	551	679	3.40E-33	0.03	0.95		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
486	1d2e	A	58	454	0			627.43	ELONGATION FACTOR TU (EF-TU); CHAIN: A, B, C, D	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL
486	1d2e	A	58	454	0	1.12	1		ELONGATION FACTOR TU (EF-TU); CHAIN: A, B, C, D	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL
486	1dar		49	192	3.40E-17	-0.05	0.19		ELONGATION FACTOR G; CHAIN: NULL;	TRANSLATIONAL GTPASE EF-G RIBOSOMAL TRANSLOCASE, TRANSLATIONAL GTPASE
487	1aca		1926	1954	0.0014	-0.46	0.11		ACYL-COENZYME A BINDING PROTEIN ACYL-COENZYME A BINDING PROTEIN (ACBP) COMPLEX WITH 1ACA 3 PALMITOYL-COENZYME A (NMR, 20 STRUCTURES) 1ACA 4	
487	1b7t	A	1	794	0			510.37	MYOSIN HEAVY CHAIN; CHAIN: A; MYOSIN REGULATORY LIGHT CHAIN; CHAIN: Y; MYOSIN ESSENTIAL LIGHT CHAIN; CHAIN: Z;	MYOSIN MYOSIN MOTOR
487	1b7t	A	5	807	0	0.41	1		MYOSIN HEAVY CHAIN; CHAIN: A; MYOSIN REGULATORY LIGHT CHAIN; CHAIN: Y; MYOSIN ESSENTIAL LIGHT CHAIN; CHAIN: Z;	MYOSIN MYOSIN MOTOR
487	1br1	A	1	765	0			524.14	MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
487	1br1	A	5	769	0	0.58	1		MYOSIN; CHAIN: A, B, C, D;	MUSCLE PROTEIN MDE; MUSCLE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
487	1br2	A	11	725	0	0.58	1		E, F, G, H; MYOSIN; CHAIN: A, B, C, D, E, F;	PROTEIN MUSCLE PROTEIN MUSCLE PROTEIN
487	1br2	A	11	739	0			470.06	MYOSIN; CHAIN: A, B, C, D, E, F;	MUSCLE PROTEIN MUSCLE PROTEIN
487	1bk	A	1394	1495	9.80E-08	-0.2	0.11		BRUTON'S TYROSINE KINASE; CHAIN: A, B;	TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE
487	1bt		1216	1306	8.40E-13	0.42	0.28		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
487	1bt		1318	1382	0.00042	-0.39	0.07		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
487	1cii		796	933	2.80E-19	0.21	-0.19		COLICIN 1A; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
487	1cii		810	979	2.80E-18	0.03	-0.19		COLICIN 1A; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
487	1cun	A	726	940	1.40E-13	0.07	-0.14		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
487	1cun	A	809	946	1.10E-14	0.27	-0.17		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
487	1dfk	A	5	807	0	0.23	1		MYOSIN HEAD; CHAIN: A; MYOSIN HEAD; CHAIN: Y; MYOSIN HEAD; CHAIN: Z;	CONTRACTILE PROTEIN MYOSIN MOTOR, CONFORMATIONAL CHANGES
487	1efl	A	1710	2002	4.20E-27	0.13	0.99		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN
487	1ez3	A	809	885	1.40E-11	0.37	-0.2		SYNTAXIN-1A; CHAIN: A, B;	ENDOCYTOSIS/EXOCYTOSIS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									C;	SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
487	1ez3	A	814	933	1.10E-16	0.3	-0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS
487	1fao	A	1215	1308	2.80E-22	0.43	0.92		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
487	1fao	A	1331	1382	7.00E-10	0.13	0.96		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
487	1fao	A	1397	1497	4.20E-10	0.19	0.36		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
487	1fb8	A	1215	1308	5.60E-22	0.54	0.99		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
487	1fb8	A	1331	1382	8.40E-10	-0.06	0.86		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
487	1fb8	A	1397	1497	1.40E-10	-0.03	0.25		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
487	1fgy	A	1215	1308	2.80E-16	0.21	0.31			TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
487	1gc7	A	1710	2044	2.80E-26	0.08	1		GRP1; CHAIN: A; RADIXIN; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN CELL ADHESION 3 SUBDOMAINS, CYTOSKELETON, CELL ADHESION
487	1lwk		2	739	0			540.6	MYOSIN; CHAIN: NULL;	CONTRACTILE PROTEIN MYOSIN, DICTYOSTELIUM, MOTOR, MANT, ATPASE, ACTIN-BINDING, 2 COILED COIL
487	1lwk		5	725	0	0.6	1		MYOSIN; CHAIN: NULL;	CONTRACTILE PROTEIN MYOSIN, DICTYOSTELIUM, MOTOR, MANT, ATPASE, ACTIN-BINDING, 2 COILED COIL
487	1mnd		1	671	0			479.56	MYOSIN; CHAIN: NULL;	CONTRACTILE PROTEIN ATPASE, MYOSIN, COILED COIL, ACTIN-BINDING, ATP-BINDING, 2 HEPTAD REPEAT PATTERN, METHYLATION, ALKYLATION, 3 PHOSPHORYLATION, CONTRACTILE PROTEIN
487	1mnd		5	671	0	0.63	1		MYOSIN; CHAIN: NULL;	CONTRACTILE PROTEIN ATPASE, MYOSIN, COILED COIL, ACTIN-BINDING, ATP-BINDING, 2 HEPTAD REPEAT PATTERN, METHYLATION, ALKYLATION, 3 PHOSPHORYLATION, CONTRACTILE PROTEIN
487	1pls		1214	1315	2.80E-17	0.11	0.46		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOMOLOGY DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105- LEHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	
487	1pls		1342	1381	5.60E-05	-0.55	0.04		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOMOLOGY DOMAIN) MUTANT IPLS 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
487	1pls		1394	1495	9.80E-12	0.02	-0.01		WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) IPLS 5 PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) IPLS 5 SOS 1; CHAIN: NULL;	
487	1pms		1211	1308	8.40E-15	0.01	-0.01			SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS; SIGNAL TRANSDUCTION
487	1pms		1331	1381	0.00014	-0.14	0.05		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS; SIGNAL TRANSDUCTION
487	1qog	A	1331	1464	7.00E-07	-0.27	0.25		INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	SIGNAL TRANSDUCTION IRS-1; BETA-SAND WHICH, SIGNAL TRANSDUCTION
487	1quu	A	797	973	1.30E-20	0.05	-0.13		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
487	2mys	A	2	801	0			419.33	MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
487	2mys	A	4	775	0	0.53	1		MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
489	1tub	A	1	440	0			727.18	TUBULIN; CHAIN: A, B;	MICROTUBULES MICROTUBULES, ALPHA-TUBULIN, BETA-TUBULIN, GTPASE HELIX
489	1tub	A	1	440	0	0.8	1		TUBULIN; CHAIN: A, B;	MICROTUBULES MICROTUBULES, ALPHA-TUBULIN, BETA-TUBULIN, GTPASE HELIX
492	1a06		16	312	1.50E-87	0.35	1		CALCIUM/CALMODULIN-	KINASE KINASE, SIGNAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
492	1a06		17	318	1.50E-87			121.63	DEPENDENT PROTEIN KINASE; CHAIN: NULL; CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	TRANSDUCTION, CALCIUM/CALMODULIN KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
492	1a60		2	316	1.70E-43			90.87	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
492	lap _m	E	1	315	0	0.41	1		TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) IAPM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (S139A\$) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 IAPM 6	
492	lap _m	E	3	333	0			158.35	TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) IAPM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (S139A\$) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 IAPM 6	
492	laql		22	314	1.00E-57			120.73	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUFOSPORINE, 2 CELL DIVISION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
492	1bi8	A	23	303	2.80E-54			117.12	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	MITOSIS, INHIBITION COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
492	1bi9	A	18	308	1.40E-59			139.32	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
492	1byg	A	18	286	1.40E-39			120.46	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUFORIN, TRANSFERASE
492	1cki	A	17	303	9.80E-51			82.9	CASEIN KINASE I DELTA; ICKI 6 CHAIN: A, B; ICKI 7	PHOSPHOTRANSFERASE PROTEIN KINASE ICKI 18
492	1cmk	E	1	315	0	0.42	1		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
492	1cmk	E	3	333	0			156.27	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
492	1ctp	E	1	315	0	0.32	1		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
492	1ctp	E	3	330	0			152.26	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
492	1f3m	C	23	303	2.80E-69	0.38	1		SUBUNIT 1CTP 4 SERINE/THREONINE- PROTEIN KINASE PAK- ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK- ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
492	1f3m	C	4	293	5.10E-69	0.21	1		SERINE/THREONINE- PROTEIN KINASE PAK- ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK- ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
492	1fgk	A	11	286	2.80E-38			123.75	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
492	1fgk	B	12	285	1.20E-40			127.9	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
492	1hcl		22	314	1.40E-60			141.29	HUMAN CYCLIN- DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
492	1ian		5	346	2.80E-45			104.86	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
492	1ir3	A	9	297	9.80E-40			105.26	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	Seqfold score	Coumpound	PDB annotation
492	1jnk		8	357	7.00E-54			127.36	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	ANALOG, ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
492	1koa		22	334	1.70E-70	0.27	1		TWITCHIN; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
492	1kob	A	1	351	3.40E-71			139.94	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
492	1kob	A	17	284	3.40E-71	0.4	1		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
492	1p38		4	350	1.40E-56			121.52	MAP KINASE P38; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
492	1phk		22	282	1.20E-81			109.51	PHOSPHORYLASE KINASE; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
492	1phk		23	279	1.20E-81	0.6	1		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
492	1pnc		18	341	5.60E-50			118.65	ERK2; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
492	1tki	A	19	334	4.20E-65			126.69	TITIN; CHAIN: A, B;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
492	1tki	A	22	274	4.20E-65	0.49	1		TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
492	3erk		11	346	4.20E-56			130.2	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
										TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
493	1av1	A	58	278	0.0042			66.14	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
493	1avj		370	440	1.70E-08	0.64	0.75		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T-CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
493	1aze	A	388	442	4.20E-19	0.47	1		GRB2; CHAIN: A; SOS; CHAIN: B;	COMPLEX (ADAPTOR PROTEIN/PEPTIDE) ASH, GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; COMPLEX (ADAPTOR PROTEIN/PEPTIDE), SH3 DOMAIN, 2 GUANINE-NUCLEOTIDE RELEASING FACTOR
493	1bbz	A	390	444	7.00E-18	0.67	0.95		ABL TYROSINE KINASE; CHAIN: A, C, E, G; PEPTIDE P41; CHAIN: B, D, F, H;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE), SIGNAL TRANSDUCTION, 2 SH3 DOMAIN
493	1cka	A	389	442	8.40E-18	0.58	0.99		COMPLEX (ONCOGENE PROTEIN/PEPTIDE) C-CRK (N-TERMINAL SH3 DOMAIN) (C-CRKSH3-N) COMPLEXED WITH ICKA 3 C3G PEPTIDE (PRO-PRO-PRO-ALA-LEU-PRO-PRO-LYS-LYS-ARG) ICKA 4	
493	1csk	A	387	442	9.80E-19	0.72	0.99		PHOSPHOTRANSFERASE C-SRC KINASE (SH3 DOMAIN) (E.C.2.7.1.12) ICSK 3	
493	1ez3	A	93	214	2.80E-06	0.22	0.05		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
493	1fio	A	166	256	0.0056	0.24	0.05		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
493	1fyn	A	385	444	2.80E-17	0.02	0.88		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
										TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
493	1gbq	A	388	442	2.80E-18	0.34	1		GRB2; CHAIN: A; SOS-1; CHAIN: B;	
493	1gbr	A	380	444	5.60E-19	0.47	1		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
493	1gri	A	272	444	1.10E-16	0.34	0.43		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
493	1hsq		383	444	2.80E-18	0.6	0.99		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
493	1qly	A	389	444	4.20E-18	0.47	0.98		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
493	1qqe	A	1	262	4.20E-07			69.94	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
493	4hek		385	444	7.00E-19	0.1	0.99		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
498	1alh	A	342	422	5.60E-35			82.45	QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
498	1alh	A	370	478	5.60E-35	0.03	1		OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, DNA-BINDING PROTEIN
498	1alh	A	398	505	1.40E-33	0.12	0.77			COMPLEX (ZINC FINGER/DNA) ZINC FINGER, DNA-BINDING PROTEIN
498	1mey	C	257	338	6.80E-49	0.38	1			COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1mey	C	285	366	1.70E-50	0.4	1			COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1mey	C	313	394	3.40E-51	0.24	1			COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1mey	C	341	422	5.10E-51	0.34	1			COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1mey	C	341	423	3.40E-51			110.98		COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1mey	C	397	477	3.40E-47	0.05	1			COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1mey	C	397	505	4.20E-36	-0.05	0.87			COMPLEX (ZINC FINGER/DNA) ZINC FINGER, DNA-BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
	y								CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1me y	C	424	505	1.00E-49	0.23	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1me y	C	452	511	1.70E-35	0.19	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1me y	G	255	282	3.40E-12	0.1	-0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1tf6	A	221	375	1.00E-33	0.06	-0.01		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
498	1tf6	A	285	447	1.40E-68			102.44	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
498	1tf6	A	286	437	1.70E-36	0.11	0.94		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
498	1tf6	A	342	487	8.50E-39	-0.02	0.92		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
	y								CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1me y	C	424	505	1.00E-49	0.23	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1me y	C	452	511	1.70E-35	0.19	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1me y	G	255	282	3.40E-12	0.1	-0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
498	1tf6	A	221	375	1.00E-33	0.06	-0.01		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
498	1tf6	A	285	447	1.40E-68			102.44	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
498	1tf6	A	286	437	1.70E-36	0.11	0.94		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
498	1tf6	A	342	487	8.50E-39	-0.02	0.92		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
498	1tf6	A	370	507	8.50E-35	0.14	0.95		TFIIA; CHAIN: A, D; 3S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
498	1ubd	C	228	338	1.00E-30	-0.02	0.05		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
498	1ubd	C	265	366	1.70E-34	0.25	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
498	1ubd	C	285	395	2.80E-56			88.23	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
498	1ubd	C	290	394	2.80E-56	0.23	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
498	1ubd	C	293	394	8.50E-35	0.36	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
498	1ubd	C	311	422	2.80E-56	0	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
498	1ubd	C	405	505	6.80E-36	-0.07	0.92		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
498	2gli	A	200	337	8.50E-33	-0.26	0.28		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
498	2gli	A	285	423	2.80E-70			97.78	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
498	2gli	A	290	422	2.80E-70	0.24	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
498	2gli	A	293	423	3.40E-33	0.36	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
498	2gli	A	313	479	1.30E-63	0.14	0.86		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
498	2gli	A	341	507	4.20E-61	0.17	0.41		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
498	2gli	A	377	504	6.80E-32	0.04	0.48		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
499	1fqv	A	28	57	0.0007	-0.78	0.52		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, I, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
499	1fs1	A	28	57	2.80E-06	-0.81	0.53		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
500	1fbv	A	866	907	1.70E-06	0.08	0.16		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
501	1bor		255	305	1.40E-13	-0.37	0.01		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
501	1chc		259	323	8.40E-17	-0.07	0.53		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
501	1chc		261	316	3.40E-16	0.02	0.69		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
501	1fbv	A	262	307	5.60E-11	-0.55	0.81		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
501	1fbv	A	263	310	1.70E-09	-0.24	1		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
501	1g25	A	259	319	7.00E-13	-0.17	0.22		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)
501	1rmd		239	333	8.40E-18	-0.11	0.94		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
501	1rmd		263	342	1.70E-09	-0.27	0.45		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
502	1c4r	A	50	224	1.40E-17	0.21	-0.11		NEUREXIN-1 BETA; CHAIN: A, B, C, D, E, F, G, H;	MEMBRANE PROTEIN LECTIN-LIKE, NEUROBIOLOGY, CELL-CELL ADHESION, CELL-CELL 2 RECOGNITION, ALTERNATIVE SPLICING, MEMBRANE PROTEIN
502	1d0s	A	1042	1380	1.10E-23	0.3	-0.2		NICOTINATE MONONUCLEOTIDE:5,6-CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
502	1d0s	A	753	1072	1.30E-20	0.51	-0.18		NICOTINATE MONONUCLEOTIDE:5,6-CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
502	1d0s	A	911	1241	1.10E-23	0.56	-0.2		NICOTINATE MONONUCLEOTIDE:5,6-CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
502	1kap	P	1076	1439	7.00E-14	0.96	-0.2		ALKALINE PROTEASE; IKAP 4 CHAIN: P, IKAP 5 TETRAPEPTIDE (GLY SER	ZINC METALLOPROTEASE P. AERUGINOSA ALKALINE PROTEASE; IKAP 6 CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
502	1kap	P	482	743	5.60E-10	1.1	-0.19		ASN SER; IKAP 9 CHAIN: I; IKAP 10	IKAP 19
502	1kap	P	530	858	8.40E-14	1.03	-0.2		ALKALINE PROTEASE; IKAP 4 CHAIN: P; IKAP 5 TETRAPEPTIDE (GLY SER ASN SER); IKAP 9 CHAIN: I; IKAP 10	ZINC METALLOPROTEASE P. AERUGINOSA ALKALINE PROTEASE; IKAP 6 CALCIUM BINDING PROTEIN IKAP 19
502	1kap	P	890	1244	1.10E-13	0.87	-0.19		ALKALINE PROTEASE; IKAP 4 CHAIN: P; IKAP 5 TETRAPEPTIDE (GLY SER ASN SER); IKAP 9 CHAIN: I; IKAP 10	ZINC METALLOPROTEASE P. AERUGINOSA ALKALINE PROTEASE; IKAP 6 CALCIUM BINDING PROTEIN IKAP 19
502	1osm	A	1004	1348	1.10E-31	1.07	-0.2		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
502	1osm	A	707	1043	1.40E-32	1.04	-0.19		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
502	1osm	A	875	1241	4.20E-27	0.87	-0.2		OMP36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
502	1pho		692	1045	1.40E-23	0.83	-0.2		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) IPHO 3	
502	1pho		872	1214	7.00E-27	1.15	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) IPHO 3	
502	1qu0	A	78	225	2.80E-13	0.51	0.1		LAMININ ALPHA2 CHAIN; CHAIN: A, B, C, D;	METAL BINDING PROTEIN BETA SANDWICH, CALCIUM-BINDING PROTEIN, METAL BINDING 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
502	2omf		842	1202	7.00E-21	1	-0.18		MATRIX PORIN OUTER MEMBRANE PROTEIN F; 2OMF 5 CHAIN: NULL; 2OMF 6	PROTEIN INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 2OMF 7 PORIN, MEMBRANE PROTEIN 2OMF 12
506	1qsm	A	227	282	0.0028	-0.12	0.06		HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE
507	1btn		82	187	1.70E-22	0.36	0.86		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
507	1btn		83	187	2.80E-24	0.38	0.78		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
507	1dro		73	192	7.00E-28			50.76	BETA-SPECTRIN; IDRO 6 CHAIN: NULL; IDRO 7	CYTOSKELETON
507	1dro		83	190	5.10E-17	0.08	0.39		BETA-SPECTRIN; IDRO 6 CHAIN: NULL; IDRO 7	CYTOSKELETON
507	1dro		92	189	7.00E-28	0.35	0.75		BETA-SPECTRIN; IDRO 6 CHAIN: NULL; IDRO 7	CYTOSKELETON
507	1fao	A	88	185	3.40E-17	0.15	-0.07		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
507	1pls		88	188	1.70E-18	0.05	0.16		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105- LEHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	
507	1pms		80	190	2.80E-14	-0.02	0.01		SOS 1; CHAIN: NULL;	SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION
508	1aoa		107	250	1.20E-32	-0.05	0.72		T-FIMBRIN; CHAIN: NULL;	ACTIN-BINDING PROTEIN ACTIN- BINDING PROTEIN, CALCIUM-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
508	1dxx	A	106	248	8.50E-30	-0.01	0.03		DYSTROPHIN; CHAIN: A, B, C, D;	BINDING, PHOSPHORYLATION STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOG DOMAIN, 2 ACTIN-BINDING, UTROPHIN
508	1qag	A	110	248	1.70E-29	0.01	0.27		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOG DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
515	1eun	A	365	562	2.80E-09	-0.06	0.09		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
515	1dn1	B	208	460	1.40E-18	-0.13	0.05		SYNTAXIN BINDING PROTEIN 1; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
515	1dn1	B	364	561	1.10E-10	-0.31	0.3		SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
515	1dn1	B	713	940	1.10E-08	-0.3	0.03		SYNTAXIN BINDING PROTEIN 1; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
515	1ez3	A	804	933	1.10E-09	0.25	0.03		SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
515	1fio	A	794	989	2.80E-05	-0.45	0.18		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
515	1quu	A	205	467	4.20E-21	-0.12	0.06		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
516	1bq0		46	124	6.80E-33			57.77	DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
516	1bq0		47	122	6.80E-33	0.45	1		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
516	1hdj		46	125	1.00E-30			52.89	HUMAN HSP40; CHAIN: NULL;	DNAK
516	1hdj		48	122	1.00E-30	0.21	1		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
522	1abr	B	378	547	1.40E-10	-0.08	0.01		COMPLEX (GLYCOSIDASE/CARBOHYDRATE) ABRIN-A COMPLEXED WITH TWO SUGAR CHAINS 1ABR 3	
522	1abr	B	412	547	6.80E-30	0.04	0.04		COMPLEX (GLYCOSIDASE/CARBOHYDRATE) ABRIN-A COMPLEXED WITH TWO SUGAR CHAINS 1ABR 3	
522	1dgg	A	444	513	0.0017	-0.22	0.13		MANNOSE RECEPTOR; CHAIN: A;	SUGAR BINDING PROTEIN BETA TREFOIL, MULTILECTIN RECEPTOR, PITUITARY HORMONES, 2 SULFATED CARBOHYDRATE TRANSFERASE
522	1ggq	A	111	333	5.10E-23	0.17	0.11		SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN CHAIN: A;	GLYCOSYLTRANSFERASE
522	1ggq	A	111	371	7.00E-45	-0.1	0		SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN CHAIN: A;	TRANSFERASE GLYCOSYLTRANSFERASE
522	1xyf	A	422	548	1.70E-31	0.08	0.96		ENDO-1,4-BETA-XYLANASE; CHAIN: A, B;	HYDROLASE XYLAN DEGRADATION
522	2aai	B	413	547	1.70E-28	0.07	0.03		GLYCOSIDASE RICIN (E.C.3.2.2.22) 2AAI 3	
523	1fdh	G	1	92	1.00E-39			112.26	OXYGEN TRANSPORT HEMOGLOBIN (DEOXY, HUMAN FETAL F=115=) 1FDHG 1 1FDHH 2	
523	1fdh	G	1	92	1.00E-39	0.29	1		OXYGEN TRANSPORT HEMOGLOBIN (DEOXY, HUMAN FETAL F=115=) 1FDHG 1 1FDHH 2	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
523	1gcv	B	1	92	7.00E-40	0.06	1		HEMOGLOBIN; CHAIN: A, C; HEMOGLOBIN; CHAIN: B, D;	OXYGEN STORAGE/TRANSPORT HEMOGLOBIN; DEOXY FORM
526	1awj		1018	1088	1.40E-18	0.45	0.15		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T- CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
526	1aze	A	1037	1087	2.80E-18	0.5	0.89		GRB2; CHAIN: A; SOS; CHAIN: B;	COMPLEX (ADAPTOR PROTEIN/PEPTIDE) ASH, GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; COMPLEX (ADAPTOR PROTEIN/PEPTIDE), SH3 DOMAIN, 2 GUANINE-NUCLEOTIDE RELEASING FACTOR
526	1b7t	A	1	739	0			335.35	MYOSIN HEAVY CHAIN; CHAIN: A; MYOSIN REGULATORY LIGHT CHAIN; CHAIN: Y; MYOSIN ESSENTIAL LIGHT CHAIN; CHAIN: Z;	MYOSIN MYOSIN MOTOR
526	1b7t	A	1	739	0	0.34	1		MYOSIN HEAVY CHAIN; CHAIN: A; MYOSIN REGULATORY LIGHT CHAIN; CHAIN: Y; MYOSIN ESSENTIAL LIGHT CHAIN; CHAIN: Z;	MYOSIN MYOSIN MOTOR
526	1br1	A	1	708	0	0.59	1		MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
526	1br1	A	1	711	0			352.11	MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
526	1br2	A	1	679	0			339.22	MYOSIN; CHAIN: A, B, C, D, E, F;	MUSCLE PROTEIN MUSCLE PROTEIN
526	1br2	A	1	679	0	0.44	1		MYOSIN; CHAIN: A, B, C, D, E, F;	MUSCLE PROTEIN MUSCLE PROTEIN
526	1dfk	A	1	739	0	0.01	1		MYOSIN HEAD; CHAIN: A; MYOSIN HEAD; CHAIN: Y; MYOSIN HEAD; CHAIN: Z;	CONTRACTILE PROTEIN MYOSIN MOTOR, CONFORMATIONAL CHANGES
526	1gbr	A	1028	1089	1.10E-19	0.45	0.72		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
526	lgfc		1035	1089	1.30E-19	0.29	0.59		3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5 ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C- TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
526	lgri	A	968	1089	8.40E-17	-0.23	0.12		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
526	lhsq		1032	1089	1.40E-18	0.24	1202.08		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
526	llvk		1	678	0	0.18	1		MYOSIN; CHAIN: NULL;	CONTRACTILE PROTEIN MYOSIN, DICTYOSTELIUM, MOTOR, MANT, ATPASE, ACTIN-BINDING, 2 COILED COIL
526	llvk		1	679	0			348.12	MYOSIN; CHAIN: NULL;	CONTRACTILE PROTEIN MYOSIN, DICTYOSTELIUM, MOTOR, MANT, ATPASE, ACTIN-BINDING, 2 COILED COIL
526	lmm _d		1	608	0			269.23	MYOSIN; CHAIN: NULL;	CONTRACTILE PROTEIN ATPASE, MYOSIN, COILED COIL, ACTIN- BINDING, ATP-BINDING, 2 HEPTAD REPEAT PATTERN, METHYLATION, ALKYLATION, 3 PHOSPHORYLATION, CONTRACTILE PROTEIN
526	lmm _d		1	608	0	0.37	1		MYOSIN; CHAIN: NULL;	CONTRACTILE PROTEIN ATPASE, MYOSIN, COILED COIL, ACTIN- BINDING, ATP-BINDING, 2 HEPTAD REPEAT PATTERN, METHYLATION, ALKYLATION, 3 PHOSPHORYLATION, CONTRACTILE PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
526	1pwt		1032	1089	7.00E-20	0.67	-1.41		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
526	1qly	A	1036	1089	4.20E-18	0.25	-1.41		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
526	1sem	A	1035	1089	4.20E-19	0.63	0.94		SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, ISEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR ISEM 19
526	2mys	A	1	731	0	-0.02	1		MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
526	2mys	A	1	737	0			267.23	MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
526	4hck		1032	1089	1.10E-18	0.32	0.18		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
528	3grx		14	96	0.0015	-0.21	0.68		GLUTAREDOXIN 3; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, THIOL-DISULFIDE OXIDOREDUCTASE, 2 THIOLTRANSFERASE, THIOREDOXIN SUPERFAMILY
528	3grx		23	89	9.80E-06	0.17	0.96		GLUTAREDOXIN 3; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, THIOL-DISULFIDE OXIDOREDUCTASE, 2 THIOLTRANSFERASE, THIOREDOXIN SUPERFAMILY
529	1b6b	B	14	159	3.40E-19	0.25	0.96		ARYALKYLAMINE N-ACETYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE ACETYLTRANSFERASE
529	1b87	A	24	184	6.80E-08	0.29	0.95		AMINOGLYCOSIDE N6'-ACETYLTRANSFERASE TYPE 1; CHAIN: A;	TRANSFERASE AAC; AMINOGLYCOSIDE 6'-N-ACETYLTRANSFERASE, ANTIBIOTIC

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
529	1ejw	A	14	159	1.20E-19	0.5	0.88		SEROTONIN N-ACETYLTRANSFERASE; CHAIN: A;	2 RESISTANCE, ACETYL COENZYME A TRANSFERASE
529	1cm0	B	36	174	2.80E-13	0.39	0.81		P300/CBP ASSOCIATING FACTOR; CHAIN: B, A;	SIGNALING PROTEIN P300/CBP ASSOCIATED FACTOR, COENZYME A, ACETYLTRANSFERASE, 2 COACTIVATOR, SIGNALING PROTEIN
529	1cm0	B	77	184	1.70E-05	0.15	0.19		P300/CBP ASSOCIATING FACTOR; CHAIN: B, A;	SIGNALING PROTEIN P300/CBP ASSOCIATED FACTOR, COENZYME A, ACETYLTRANSFERASE, 2 COACTIVATOR, SIGNALING PROTEIN
529	1qsm	A	11	156	1.50E-13	0.13	0.33		HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE
529	1qsm	A	12	165	4.20E-19	0.15	0.23		HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE
529	1qst	A	79	183	3.40E-07	-0.06	0.19		TGCN5 HISTONE ACETYLTRANSFERASE; CHAIN: A;	TRANSFERASE HISTONE ACETYLTRANSFERASE, GCN5-RELATED N-ACETYLTRANSFERASE, 2 COA BINDING PROTEIN
529	1ygh	A	80	179	1.00E-05	0.09	0.04		TRANSCRIPTIONAL ACTIVATOR GCN5; CHAIN: A, B;	GENE REGULATION ADA4; TRANSCRIPTIONAL REGULATION, HISTONE ACETYLATION, N-2 ACETYLTRANSFERASE, GCN5 RELATED N-ACETYLTRANSFERASE FAMILY, 3 GENE REGULATION
534	1clg	A	3	296	1.50E-54	-0.48	1		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
534	1clg	A	3	245	3.40E-49	-0.17	0.64		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
534	1clg	A	3	248	5.10E-53	-0.17	0.94		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
535	1clg	A	3	296	1.50E-54	-0.48	1		TROPOMYOSIN; CHAIN: A;	CONTRACTILE PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
535	1c1g	A	3	245	3.40E-49	-0.17	0.64		B, C, D	TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
535	1c1g	A	3	248	5.10E-53	-0.17	0.94		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN
									TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN	
									TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN
538	1a4y	A	6	306	4.20E-25	0.29	0.47		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPIPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
538	1a9n	A	136	297	2.80E-22	0.75	1		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
538	1a9n	A	164	306	4.20E-18	0.42	0.45		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
538	1a9n	A	210	284	0.00017	0.59	0.29		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
538	1a9n	A	40	144	3.40E-06	-0.09	0.12		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
538	1a9n	C	136	301	5.60E-23	0.65	0.9		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
538	1a9n	C	210	284	0.00017	0.48	0.29		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
538	1a9n	C	40	144	3.40E-06	0.1	0.03		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
538	1d0b	A	127	286	1.70E-22	0.41	0.8		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
538	1d0b	A	183	350	1.00E-16	0.19	0.21		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
538	1d0b	A	3	162	5.10E-24	0.3	0.11		INTERNALIN B; CHAIN: A;	ADHESION CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
538	1d0b	A	32	191	1.00E-25	0.05	0.15		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
538	1d0b	A	57	212	8.50E-25	0.17	0.22		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
538	1dce	A	7	130	1.20E-09	0.02	-0.14		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
538	1ds9	A	16	143	6.80E-13	-0.03	0.16		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2
538	1fo1	A	52	120	1.00E-06	-0.32	0.13		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	CHLAMYDOMONAS, FLAGELLA RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
538	1fo1	B	227	290	1.70E-07	-0.1	0.03		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
538	1fo1	B	52	120	1.00E-06	-0.41	0.1		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
538	1fqv	A	111	284	5.10E-13	0.63	0.49		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
538	1fqv	A	9	339	2.80E-17	0.08	-0.09		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F;	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
538	1fs2	A	111	284	5.10E-13	0.13	0.24		H, I, L, N, P; SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
538	1fs2	A	84	306	1.30E-23	0.29	0		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
538	1yrg	A	86	291	2.80E-22	0.26	-0.11		GTPASE-ACTIVATING PROTEIN RNAI_SCHPO; CHAIN: A, B;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
538	2bnh		63	311	1.40E-32	0.43	0.22		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIREDIAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE- RICH REPEATS
539	1d2r	A	35	359	0	0.54	1		TRYPTOPHANYL TRNA SYNTHETASE: CHAIN: A, B, C, D, E, F;	LIGASE TRPRS; CLASS I TRNA SYNTHETASE, AARS, INDUCED FIT, TRPRS
540	1d06	A	274	371	4.20E-17	0.23	0.23		NITROGEN FIXATION REGULATORY PROTEIN FIXL; CHAIN: A;	SIGNALING PROTEIN OXYGEN SENSOR, HISTIDINE KINASE, PAS, HIGH-RESOLUTION, TWO-2 COMPONENT SYSTEM
541	1aew		30	199	7.00E-84			194.39	FERRUTIN; CHAIN: NULL;	IRON STORAGE IRON STORAGE, MULTIGENE FAMILY, ACETYLATION
541	1aew		30	199	7.00E-84	0.36	1		FERRUTIN; CHAIN: NULL;	IRON STORAGE IRON STORAGE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
541	1mfr	A	29	199	5.60E-88			221.42	M FERRITIN; CHAIN: A,B,C,D,E,F,G,H,I,J,K,L,M,N,O,P,Q,R,S,T,U,V,W,X;	MULTIGENE FAMILY, ACETYLATION IRON STORAGE IRON STORAGE, DIIRON
541	1mfr	A	30	199	5.60E-88	0.53	1		M FERRITIN; CHAIN: A,B,C,D,E,F,G,H,I,J,K,L,M,N,O,P,Q,R,S,T,U,V,W,X;	IRON STORAGE IRON STORAGE, DIIRON
541	2fha		29	200	1.40E-75			284.09	FERRITIN; CHAIN: NULL;	IRON STORAGE IRON STORAGE
541	2fha		29	200	1.40E-75	0.5	1		FERRITIN; CHAIN: NULL;	IRON STORAGE IRON STORAGE
541	2fha		29	200	1.00E-74	0.5	1		FERRITIN; CHAIN: NULL;	IRON STORAGE IRON STORAGE
546	1a58		1	162	5.10E-29			94.49	CYCLOPHILIN; CHAIN: NULL;	ISOMERASE ISOMERASE, PPIASE
546	1awq	A	1	163	5.10E-38			89.5	CYCLOPHILIN A; CHAIN: A; PEPTIDE FROM THE HIV-1 CAPSID PROTEIN; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
546	1awq	A	2	160	5.10E-38	0.7	1		CYCLOPHILIN A; CHAIN: A; PEPTIDE FROM THE HIV-1 CAPSID PROTEIN; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
546	1clh		1	166	8.40E-39			69.6	ISOMERASE(PEPTIDYL-PROLYL CIS-TRANS) CYCLOPHILIN (NMR, 12 STRUCTURES) 1CLH 3	
546	1clh		3	163	8.40E-39	0.28	0.46		ISOMERASE(PEPTIDYL-PROLYL CIS-TRANS) CYCLOPHILIN (NMR, 12 STRUCTURES) 1CLH 3	
546	1eyn	A	1	171	5.10E-34			103.11	CYCLOPHILIN B; ICYN 6 CHAIN: A; ICYN 7 [D-(CHOLINYL)ALA]8- CYCLOSPORIN; ICYN 10 CHAIN: C; ICYN 11	COMPLEX (ISOMERASE/IMMUNOSUPPRESSANT) CYCLOSPORIN, ISOMERASE, ROTAMASE, SIGNAL ICYN 19
546	1eyn	A	2	160	5.10E-34	0.52	1		CYCLOPHILIN B; ICYN 6 CHAIN: A; ICYN 7 [D-(CHOLINYL)ALA]8- CYCLOSPORIN; ICYN 10 CHAIN: C; ICYN 11	COMPLEX (ISOMERASE/IMMUNOSUPPRESSANT) CYCLOSPORIN, ISOMERASE, ROTAMASE, SIGNAL ICYN 19
546	1dy _w	A	2	160	1.70E-34	0.62	1		CYCLOPHILIN 3; CHAIN: A;	ISOMERASE(PEPTIDYL-PROLYL CIS-TRANS) PEPTIDYL-PROLYL CIS-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
546	1lop	A	2	163	7.00E-41			69.67	CYCLOPHILIN A; CHAIN: A; SUCCINYL-ALA-PRO-ALA-P- NITROANILIDE; CHAIN: B;	TRANS ISOMERASE 3, ISOMERASE, ROTAMASE
546	1lop	A	3	162	7.00E-41	0.47	0.98		SUCCINYL-ALA-PRO-ALA-P- NITROANILIDE; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) ISOMERASE, ROTAMASE, COMPLEX (ISOMERASE/PEPTIDE)
546	1qng	A	2	160	6.80E-33	0.56	1		CYCLOPHILIN A; CHAIN: A; SUCCINYL-ALA-PRO-ALA-P- NITROANILIDE; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) ISOMERASE, ROTAMASE, COMPLEX (ISOMERASE/PEPTIDE)
546	1qoi	A	2	160	1.70E-31	0.57	1		CYCLOPHILIN; CHAIN: A; CYCLOSPORIN A; CHAIN: D;	PEPTIDYLPROLYL CIS-TRANS ISOMERASE; CYCLOPHILIN A, CYCLOSPORIN A, PEPTIDYL CIS- TRANS ISOMERASE
546	1qoi	A	7	156	2.80E-36	0.31	0.98		SNUCYP-20; CHAIN: A;	ISOMERASE USA-CYP; SNUCYP-20, CYCLOPHILIN, SNRNP, SPLICEOSOMAL
546	2rmc	A	2	160	3.40E-31	0.6	1		COMPLEX (ISOMERASE/IMMUNOSUPP RESSANT) CYCLOPHILIN C COMPLEXED WITH CYCLOSPORIN A 2RMC 3	ISOMERASE USA-CYP; SNUCYP-20, CYCLOPHILIN, SNRNP, SPLICEOSOMAL
546	2rmc	A	2	172	8.40E-41			94.18	COMPLEX (ISOMERASE/IMMUNOSUPP RESSANT) CYCLOPHILIN C COMPLEXED WITH CYCLOSPORIN A 2RMC 3	
546	2rmc	A	6	171	8.40E-41	0.39	1		COMPLEX (ISOMERASE/IMMUNOSUPP RESSANT) CYCLOPHILIN C COMPLEXED WITH CYCLOSPORIN A 2RMC 3	
548	1sig		219	335	0.0028	0.33	0.01		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
549	1bor		319	363	3.40E-06	-0.43	0.03		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
549	1bor		321	366	9.80E-09	-0.5	0.16		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
549	1chc		321	370	3.40E-12	-0.21	0.8		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
549	1dt4	A	39	104	2.80E-14	0.49	0.98		NEURO-ONCOLOGICAL VENTRAL ANTIGEN 1; CHAIN: A;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTIF
549	1dtj	A	39	104	2.80E-14	0.42	0.95		RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF
549	1dtj	B	39	106	2.80E-05	0.44	0.88		RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF
549	1dtj	C	39	104	4.20E-16	0.3	0.99		RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF
549	1dtj	D	39	104	2.80E-15	0.51	0.99		RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF
549	1ec6	A	39	109	8.40E-15	0.66	1		RNA-BINDING PROTEIN NOVA-2; CHAIN: A, B; 20-MER RNA HAIRPIN; CHAIN: C, D;	RNA BINDING PROTEIN/RNA ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN; KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTIF, PROTEIN/RNA 2 STRUCTURE
549	1fbv	A	320	370	3.40E-13	0.28	0.71		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
549	1g25	A	317	363	0.00068	-0.37	0.27		CDK-ACTIVATING KINASE	METAL BINDING PROTEIN RING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
549	1g25	A	321	365	1.40E-09	-0.18	0.25		ASSEMBLY FACTOR MATI; CHAIN: A;	FINGER PROTEIN MATI; RING FINGER (C3HC4)
549	1rmd		312	363	5.10E-12	0.16	0.19		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)
549	1vig		36	104	4.20E-16	0.69	1		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
553	1d2h	A	50	165	3.40E-15	-0.04	0.29		VIGILIN; 1VIG 5 CHAIN: NULL; 1VIG 6	RIBONUCLEOPROTEIN RNA-BINDING PROTEIN 1VIG 19
553	1dus	A	51	166	8.50E-09	0.38	1		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
553	1g6q	1	34	164	5.60E-07	-0.12	0.53		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
553	1vid		48	188	4.20E-09	-0.07	0.11		HNRNP ARGinine N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6; CATECHOL O-METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER TRANSFERASE (METHYLTRANSFERASE) COMIT; TRANSFERASE, METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION
553	1xva	A	28	165	5.10E-16	-0.04	0.06		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B;	METHYLTRANSFERASE GNMT, S-ADENOSYL-L-METHIONINE; GLYCINE METHYLTRANSFERASE
554	1a1h	A	410	490	1.70E-23	-0.28	0.01		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
554	1a1h	A	446	547	8.50E-25	-0.43	0.01		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
554	1mey	G	1006	1032	1.00E-10	0.14	-0.19		BINDING SITE; CHAIN: B, C; DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
554	1mey	G	443	470	1.70E-12	0.27	0.52		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
554	1mey	G	960	985	5.10E-09	-0.21	0.04		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
554	1f3	A	366	470	3.40E-13	-0.03	0.04		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
554	2adr		409	472	5.10E-13	0.04	0.24		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
554	2adr		494	553	1.70E-15	-0.35	0		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
554	2drp	A	401	472	2.80E-11	0.01	0.89		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
555	1erj	A	30	295	3.40E-15	-0.15	0		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA- PROPELLER
555	1got	B	136	352	1.70E-11	0.11	-0.13		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-	COMPLEX (GTP- BINDING/TRANSDUCER) BETAI,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
557	1c4o	A	175	317	3.40E-14	0.1	0.59		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRBC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN
557	1d2m	A	175	317	3.40E-14	0.01	0.95		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
557	1d9x	A	123	379	8.40E-47	0.06	0.64		EXCINUCLEASE UVRBC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
557	1d9x	A	175	317	1.50E-16	-0.03	0.87		EXCINUCLEASE UVRBC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
557	1fuk	A	213	374	8.50E-45	0.8	1		EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A, HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN
557	1fuu	A	1	204	1.70E-55	0.74	1		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
557	1fuu	B	1	374	0	0.64	1		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
557	1hei	A	236	310	1.70E-06	0.39	0.19		HCV HELICASE; CHAIN: A, B;	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE
557	1hei	A	40	316	5.60E-09	-0.35	0		HCV HELICASE; CHAIN: A, B;	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE
557	1hei	B	236	310	1.70E-06	-0.11	0.05		HCV HELICASE; CHAIN: A, B;	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE
557	1qde	A	1	203	1.70E-52	0.84	1		TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	GENE REGULATION EIF4A; TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMILY
558	1d2h	A	65	195	1.40E-18	0.27	0.95		GLYCINE N-	TRANSFERASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
558	1d2h	A	67	223	2.80E-13	-0.17	0.19		METHYLTRANSFERASE; CHAIN: A, B, C, D;	METHYLTRANSFERASE
558	1dus	A	68	187	1.40E-12	0.35	0.89		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D; MJ0882; CHAIN: A;	TRANSFERASE METHYLTRANSFERASE
558	1dus	A	83	213	2.80E-14	0.25	0.93		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
558	1g6q	1	43	195	1.70E-26	0.11	0.31		HNRNP ARGinine N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
558	1xva	A	43	195	5.10E-21	-0.08	0.72		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
558	1yub		71	157	1.20E-06	0.44	0.06		RRNA METHYLTRANSFERASE; CHAIN: NULL;	METHYLTRANSFERASE GNMT, S-ADENOSYL-L-METHIONINE; GLYCINE METHYLTRANSFERASE
558	2adm	A	62	189	1.20E-08	0.09	0.48		ADENINE-N6-DNA-METHYLTRANSFERASE TAQI; CHAIN: A, B;	METHYLTRANSFERASE ERMAM; METHYLTRANSFERASE, ERM, ERMAM, MLS ANTIBIOTICS, NMR, 2 RRNA
559	1gwz		225	301	4.20E-05	-0.17	0.25		SHP-1; CHAIN: NULL;	METHYLTRANSFERASE TRANSFERASE, METHYLTRANSFERASE, RESTRICTION SYSTEM
559	1mkp		158	298	3.40E-39			137.8	PYSTI; CHAIN: NULL;	HYDROLASE PROTEIN-TYROSINE PHOSPHATASE; HYDROLASE, PROTEIN TYROSINE PHOSPHATASE, CATALYTIC DOMAIN, 2 WPD LOOP, SH2 DOMAIN
559	1mkp		159	287	3.40E-39	0.88	1		PYSTI; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
559	1vhr	A	135	307	1.10E-34			96.19	HUMAN VHI-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B; HUMAN VHI-RELATED	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
559	1vhr	A	142	298	1.10E-34	0.78	1			HYDROLASE VHR; HYDROLASE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
559	1vhr	A	146	282	1.00E-32	0.29	1		DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B; HUMAN VHI-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B;	PROTEIN DUAL-SPECIFICITY PHOSPHATASE HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE
566	1alh	A	188	248	6.80E-22	0.4	0.77		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
566	1alh	A	194	276	1.50E-28	0.03	0.83		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
566	1alh	A	194	278	1.50E-28			56.74	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
566	1alh	A	222	288	1.20E-24	-0.45	0.86		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
566	1mey	C	187	246	6.80E-36	0.07	0.69		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
566	1mey	C	193	276	5.10E-49	0.08	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
566	1mey	C	193	277	5.10E-49			69.14	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
566	1mey	C	221	288	3.40E-40	-0.37	0.46		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
566	1mey	G	219	246	1.70E-13	-0.03	0.92		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
566	1tf3	A	193	280	6.80E-18			50.62	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
566	1tf3	A	194	276	6.80E-18	-0.15	0.01		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
566	1tf6	A	198	277	1.40E-20	-0.28	0.16		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
566	1ubd	C	167	277	6.80E-29			56.56	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
566	1ubd	C	186	276	6.80E-29	-0.32	0.89		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
566	1ubd	C	201	284	5.10E-27	-0.02	0.88		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
566	2gli	A	133	278	1.50E-26			57.42	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
566	2gli	A	188	278	1.50E-26	0.23	0.72		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
571	1b3u	A	1	605	1.70E-40			161.25	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
571	1b3u	A	9	605	1.70E-40	-0.03	0.71		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
571	1ee4	A	144	602	1.30E-43	0.42	1		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
571	1ee4	A	18	459	1.40E-31	-0.06	0.83		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
571	1ee4	A	184	601	1.70E-37	0.44	1		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
571	1ee4	A	7	390	3.40E-28	0.34	1		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
571	1ial	A	304	603	5.10E-21	0.38	0.96		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
571	1ial	A	33	475	1.40E-32			152.5	IMPORTIN ALPHA; CHAIN: A;	ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
571	1ial	A	530	607	1.70E-09	0.26	0.19		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
571	1ial	A	7	390	1.40E-32	0.18	0.88		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
571	1ibr	B	225	606	6.80E-13	-0.01	0.4		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
571	1ibr	B	3	97	5.10E-12	0.11	-0.09		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
571	1qbk	B	6	605	3.40E-49	0.01	0.74		KARYOPHERIN BETA2; CHAIN: B; RAN; CHAIN: C;	NUCLEAR TRANSPORT PROTEIN COMPLEX HEAT REPEATS, NUCLEAR TRANSPORT PROTEIN COMPLEX
571	1qgr	A	3	474	6.80E-23	-0.16	0.16		IMPORTIN BETA SUBUNIT; CHAIN: A; IMPORTIN ALPHA-2 SUBUNIT; CHAIN: B;	TRANSPORT RECEPTOR KARYOPHERIN BETA-1, NUCLEAR FACTOR P97, IMPORTIN IMPORTIN ALPHA-2 SUBUNIT, KARYOPHERIN ALPHA-2 TRANSPORT RECEPTOR, NUCLEAR IMPORT, HEAT MOTIF, NLS-BINDING
571	2bct		8	500	1.40E-22	0.29	0.64		BETA-CATENIN; CHAIN:	STRUCTURAL PROTEIN ARMADILLO

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
571	2bet		89	607	6.80E-44			160.13	NULL; BETA-CATENIN; CHAIN: NULL;	REPEAT, BETA-CATENIN, STRUCTURAL PROTEIN
571	2bet		9	431	8.40E-25	0.39	1		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-CATENIN, STRUCTURAL PROTEIN
571	2bet		91	607	6.80E-44	0.31	0.94		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-CATENIN, STRUCTURAL PROTEIN
571	3bet		1	386	6.80E-18	0.57	-1.41		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
571	3bet		13	476	1.40E-31			141.33	BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
571	3bet		138	604	5.10E-36	0.45	1202.08		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
571	3bet		51	430	1.40E-31	0.35	1		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
572	1av1	A	23	219	5.60E-11			67.34	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
572	1cun	A	6	219	2.80E-12			62.14	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
572	1quu	A	3	245	1.40E-13			67.92	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
572	1sig		31	191	2.80E-09	-0.28	0.07		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
573	1av1	A	20	137	7.00E-13	0.52	-0.18		APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT- ACTIVATION
573	1cii		7	175	4.20E-16	0.06	-0.2		COLICIN 1A; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
573	1cun	A	1	175	5.60E-12	0.5	-0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
573	1cun	A	6	125	7.00E-15	0.57	-0.12		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
573	1dg3	A	16	140	1.40E-10	0.43	-0.13		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE- BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
573	1dn1	B	4	145	8.40E-14	0.39	-0.17		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
573	1dn1	B	8	175	1.40E-11	0.31	-0.19		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
573	1ez3	A	14	129	1.10E-16	0.43	-0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
573	1f5n	A	11	145	4.20E-11	0.29	-0.19		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY. GMPNP, GPPNHP.

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
573	1qge	A	6	146	1.40E-12	0.2	-0.2		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
573	1quu	A	1	101	5.60E-12	0.4	-0.2		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
573	1quu	A	6	250	1.40E-19			53.17	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
573	1quu	A	7	174	1.40E-19	0.36	-0.18		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
573	2trc	P	7	144	8.40E-11	0.08	-0.19		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
574	1crz	A	110	358	9.80E-18	0.47	0.22		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
574	1crz	A	172	466	5.60E-16	0.37	0.1		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
574	1crz	A	262	484	4.20E-15	0.41	0		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
574	1crz	A	353	476	5.10E-05	-0.14	0.22		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
574	1crz	A	97	209	1.40E-09	0.22	-0.12		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
574	1erj	A	109	484	5.60E-91	0.14	-0.14		TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
574	1erj	A	193	484	1.70E-76	0.8	1		TRANSCRIPTIONAL	TRANSCRIPTION INHIBITOR BETA-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
574	1ej	A	48	356	1.70E-67	0.46	1		REPRESSOR TUP1; CHAIN: A, B, C; TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	PROPELLER TRANSCRIPTION INHIBITOR BETA-PROPELLER
574	1got	B	101	400	3.40E-71	0.95	1		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
574	1got	B	15	273	1.00E-50	0.7	1		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
574	1got	B	190	483	6.80E-79	0.79	1		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
574	1got	B	45	315	3.40E-55	0.43	0.99		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
574	1got	B	65	400	3.40E-71			150.13	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
										SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
574	1qfn	A	111	172	0.00056	-0.33	0.05		PROLYL OLIGOPEPTIDASE; CHAIN: A;	HYDROLASE PROLYL ENDOPEPTIDASE, POST-PROLINE CLEAVING PROLYL OLIGOPEPTIDASE, AMNESIA, ALPHA/BETA-HYDROLASE, BETA-2 PROPELLER
574	1qks	A	104	478	5.60E-79	0.43	-0.19		CYTOCHROME C D1 NITRITE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE ENZYME, NITRITE REDUCTASE, OXIDOREDUCTASE, DENITRIFICATION, 2 ELECTRON TRANSPORT, PERIPLASMIC
575	1cii		49	648	1.70E-10			98.21	COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
577	1dfn	A	72	101	1.10E-12			59.92	DEFENSIN DEFENSIN /HNP\$-3 1DFN 3	
577	1dfn	A	73	101	1.10E-12	-0.35	1		DEFENSIN DEFENSIN /HNP\$-3 1DFN 3	
577	1dfn	A	73	101	5.10E-11	-0.35	1		DEFENSIN DEFENSIN /HNP\$-3 1DFN 3	
578	1bih	A	30	435	1.70E-47			111.17	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
578	1bih	A	32	416	1.70E-47	0	0.05		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
578	1bj8		344	434	5.60E-11	0.22	-0.08		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
578	1cdy		49	220	1.40E-19	0.43	-0.01		T-CELL SURFACE GLYCOPROTEIN CD4;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: NULL;	TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
578	1cfb		252	435	7.00E-20	0.25	0.39		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5 AXONIN-1; CHAIN: A;	
578	1cs6	A	137	522	1.40E-48	0.09	-0.11		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
578	1cs6	A	32	436	1.40E-50	0.06	0		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
578	1ct8	A	140	328	6.80E-13	0.11	-0.15		7C8 FAB FRAGMENT; SHORT CHAIN; CHAIN: A, C; 7C8 FAB FRAGMENT; LONG CHAIN; CHAIN: B, D	IMMUNE SYSTEM ABZYME TRANSITION STATE ANALOG, IMMUNE SYSTEM
578	1evs	C	134	340	1.40E-44	0.1	-1.41		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
578	1evs	D	31	225	3.40E-28	0.18	0.43		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
578	1evs	D	36	220	1.40E-30	0.1	0.34		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
578	1epf	A	33	214	5.60E-30	0.16	0.99		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
578	1ev2	E	38	220	4.20E-30	0.09	0.25		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
578	1ev2	G	36	228	2.80E-31	-0.06	0.48		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
578	1evt	C	29	220	5.60E-28	0.03	0.01		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
578	1f6f	B	267	436	1.40E-11	0.29	0.17		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
578	1f8g	A	27	131	6.80E-18	0.06	-0.05		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
578	1fnf		264	432	5.60E-15	0.24	0.46		FIBRONECTIN; IFNF 6 CHAIN: NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
578	1fnh	A	264	432	1.40E-12	0.24	0.04		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
578	1hnf		47	211	1.40E-18	0.3	0.29		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (HUMAN) IFNF 3	
578	1hng	A	143	292	4.20E-14	0.05	-0.12		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) IHNG 3	
578	1hng	A	49	227	2.80E-24	0.15	0.15		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) IHNG 3	
578	1igy	B	34	454	3.40E-10			95.64	IGG1 INTACT ANTIBODY	IMMUNOGLOBULIN INTACT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
578	1itb	B	52	338	6.80E-34	0.03	-0.12		MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION COMPLEX
578	1mc o	H	32	423	3.40E-10			96.36	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	(IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
578	1mfh		264	432	1.30E-17	0.39	0.33		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
578	1nct		139	227	1.40E-18	0.29	0.88		FIBRONECTIN; CHAIN: NULL; TITIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2
578	1nct		31	132	4.20E-15	0.06	-0.06		TITIN; CHAIN: NULL;	IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
578	1nct		31	132	6.80E-15	0.13	-0.13		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2
578	1qg3	A	251	450	1.40E-20	0.3	0.52		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	MUSCLE PROTEIN STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
578	1qr4	A	264	435	2.80E-17	0.52	0.82		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
578	1tnm		139	227	7.00E-18	0.39	0.89		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
578	1tnm		33	132	8.40E-15	-0.04	0.03		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
578	1ttf		346	434	1.40E-10	0.2	0.05		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	
578	1wio	A	49	281	2.80E-20	0.04	-0.12		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
578	1wit		139	226	2.80E-17	0.52	0.78		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
578	1wit		31	132	2.80E-15	0.23	0.1		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
578	1www	X	142	228	5.60E-18	0.02	-0.01		NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	NERVE GROWTH FACTOR/TRKA COMPLEX BETA-NGF; COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA COMPLEX
578	1zxq		31	228	1.10E-30	0.18	0.23		INTERCELLULAR ADHESION MOLECULE-2; CHAIN: NULL;	CELL ADHESION ICAM-2; IMMUNOGLOBULIN FOLD, CELL ADHESION, GLYCOPROTEIN, 2 TRANSMEMBRANE, REPEAT, SIGNAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
578	2dli	A	30	220	2.80E-25	0.25	-0.02		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
578	2fcb	A	31	228	2.80E-33	0.1	0.66		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
578	2fnb	A	343	435	1.40E-12	0.45	-0.12		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
578	2hft		264	436	2.80E-12	0.13	-0.08		HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NULL; 2HFT 5	COAGULATION FACTOR
578	2ncm		139	227	5.60E-18	0.64	0.98		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
578	3hhr	B	264	436	5.60E-17	0.06	-0.09		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	
578	3ncm	A	139	220	4.20E-18	0.06	0.31		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
578	3ncm	A	32	134	7.00E-17	0.04	0.06		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
579	1chc		61	103	1.00E-09	-0.56	0.01		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
579	1.00 E+53	A	51	102	0.00051	0	0.19		STRUCTURE) ICHC 4 TFIIH P44 SUBUNIT; CHAIN: A;	TRANSCRIPTION FACTOR BTF2 P44 SUBUNIT; BASIC TRANSCRIPTION FACTOR, ZINC BINDING PROTEIN
579	1rmd		223	268	0.0037	-0.01	0.33		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
579	1rmd		59	92	0.0007	-0.78	0.29		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
579	1rmd		63	128	3.40E-07	0.01	0.13		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
580	1a25	A	1329	1443	1.70E-30	0.83	0.94		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING
580	1byn	A	1325	1442	1.70E-23	0.06	0.52		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE,
580	1c1y	A	1342	1444	1.70E-15	0.05	0.13		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	ENDOCYTOSIS/EXOCYTOSIS HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
580	1dsy	A	1329	1443	3.40E-31	0.61	0.98		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
580	1e7u	A	214	1175	0	0.15	-1202.08		PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT; CHAIN: A;	PHOSPHATIDYL SERINE, PROTEIN KINASE C
580	1e8y	A	297	1175	0	0.15	-1.41		PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT; CHAIN: A;	PHOSPHOINOSITIDE 3-KINASE GAMMA PTDINS-3-KINASE P110, PI3K, PI 3K; PHOSPHOINOSITIDE 3-KINASE GAMMA, SECONDARY MESSENGER 2 GENERATION, PI3K, PI 3K, WORTMANNIN
580	1rlw		1342	1444	1.70E-15	-0.02	0.64		PHOSPHOLIPASE A2; CHAIN: NULL;	PHOSPHOINOSITIDE 3-KINASE GAMMA PTDINS-3-KINASE P110, PI3K; PHOSPHOINOSITIDE 3-KINASE GAMMA, SECONDARY MESSENGER 2 GENERATION, PI3K, PI 3K
580	1rsy		1321	1442	8.50E-24	0.06	0.59		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
580	3rpb	A	1328	1441	5.10E-29	0.1	0.39		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
585	1dg3	A	6	577	0	0.27	-0.2		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE- BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
585	1f5n	A	7	577	0	0.47	-0.2		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, GMPPNP, GPPNHP.
586	3pm _g	A	46	604	0	0.29	-0.2		ALPHA-D-GLUCOSE-1,6-BISPHOSPHATE; 3PMG 4 CHAIN: A, B; 3PMG 5	PHOSPHOTRANSFERASE PHOSPHOGLUCOMUTASE; 3PMG 6
586	3pm _g	A	53	611	0			129.26	ALPHA-D-GLUCOSE-1,6-BISPHOSPHATE; 3PMG 4	PHOSPHOGLUCOMUTASE 3PMG 13 PHOSPHOTRANSFERASE PHOSPHOGLUCOMUTASE; 3PMG 6

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A, B; 3PMG 5	PHOSPHOGLUCOMUTASE 3PMG 13
587	1bor		16	59	8.50E-06	-0.73	0.25		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2
587	1bor		17	56	8.40E-08	-0.62	0.11		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2
587	1hc		16	60	8.50E-15	0.24	0.98		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	TRANSCRIPTION REGULATION
587	1bv	A	18	66	1.70E-10	0.25	0.9		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
587	1g25	A	17	64	8.40E-08	0.19	0.48		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
587	1g25	A	18	72	1.20E-05	-0.44	0.09		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
592	1a7i		536	592	9.80E-17	-0.16	0.62		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
592	1a7i		597	662	1.40E-11	-0.1	0		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
592	1b8t	A	597	659	4.20E-11	-0.11	0.18		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
592	1ctf		596	659	1.10E-12	-0.11	0.16		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
592	1cxx	A	535	592	1.40E-16	0.43	0.8		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
592	1cxx	A	595	661	1.10E-13	-0.27	0.23		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
592	1iml		537	609	1.30E-19	-0.42	0.29		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
592	1iml		596	663	4.20E-13	0.15	0.07		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
592	1mey	G	367	395	1.20E-10	0.16	-0.19		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
593	1a5e		315	370	0.00014	0.1	0.72		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
593	1awc	B	315	369	0.00014	0.35	0.1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABPBETA1: COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
593	1bd8		315	370	0.00011	0.28	0.76		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
593	1b17	B	315	367	9.80E-05	0.02	0.82		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
593	1blx	B	315	367	0.00011	0.23	0.84		CYCLIN-DEPENDENT KINASE 6; CHAIN: A;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									P19INK4D; CHAIN: B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
593	1bix	B	315	370	0.00011	0.42	0.76		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
593	1d9s	A	315	370	1.40E-05	-0.02	0.21		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
593	1deq	A	315	370	8.40E-05	0.4	0.76		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
593	1likn	D	315	370	0.00014	0.31	0.98		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
593	1nfi	E	315	381	2.80E-06	0.25	0.59		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
594	1a06		19	302	5.10E-90	0.15	1		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
594	1apm	E	25	318	0	0.23	1		TRANSFERASE(PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
594	lapm	E	5	325	0			125.65	IAPM 6 TRANSFERASE(PHOSPHOTRANSFERASE) \$C\$-AMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) IAPM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (SI39A\$) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 IAPM 6	
594	laql		27	309	1.40E-60			120.88	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
594	lbkx	A	22	325	7.00E-56			127.11	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
594	lcmk	E	1	328	0			127.4	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
594	lcmk	E	25	318	0	0.33	1		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
594	lctp	E	2	328	0			127.61	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
594	1ctp	E	25	318	0	0.25	1		SUBUNIT ICTP 4	
									TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	
594	1dn1	B	442	600	4.20E-12	0.06	-0.11		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B; SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
594	1ez3	A	452	592	1.40E-08	0.1	-0.19			ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
594	1ez3	A	486	617	2.80E-09	0.16	-0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
594	1f3m	C	14	302	5.60E-86	0.5	1		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
594	1f3m	C	4	300	1.20E-67	0.43	-1202.08		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
594	1fgk	A	20	287	5.10E-34			125.79	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
594	1fgk	B	11	286	1.20E-40			130.09	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
594	1hcl		25	284	6.80E-62	0.48	1		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	RECEPTOR, PHOSPHOTRANSFERASE PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
594	1hcl		27	312	6.80E-62			137.2	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
594	1koa		20	285	3.40E-71	0.5	1		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN; INTRASTERIC REGULATION
594	1kob	A	20	284	1.70E-71	0.48	1		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN; INTRASTERIC REGULATION
594	1p38		6	356	1.20E-51			130.84	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
594	1phk		19	285	6.80E-88			127.79	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE- PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
594	1phk		24	282	6.80E-88	0.53	1		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE- PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
594	3erk		10	325	8.50E-50			122.57	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
596	1a06		140	438	1.00E-66	0	1202.08		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
596	1a6o		234	351	4.20E-07	-0.44	0.22		PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
596	1apm	E	122	434	3.40E-100	-0.03	0.49		TRANSFERASE(PHOSPHOTRANSFERASE) \$C\$/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C\$/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (S139A) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
596	1aql		146	399	8.50E-49	0.03	0.76		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
596	1bi8	A	149	397	8.50E-32	-0.06	0.05		CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
596	1bi9	A	149	398	1.70E-35	0.2	0.3		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
596	1byg	A	146	344	3.40E-30	0.01	0.46		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
596	1cki	A	198	351	5.60E-09	-0.08	0.34		CASEIN KINASE I DELTA;	PHOSPHOTRANSFERASE PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
596	1cm8	A	163	396	1.50E-31	0.32	0.09		ICK16 CHAIN: A, B; ICK17 PHOSPHORYLATED MAP KINASE P38-GAMMA; CHAIN: A, B;	KINASE ICK18 TRANSFERASE STRESS-ACTIVATED PROTEIN KINASE-3, ERK6, ERK5; P38-GAMMA, GAMMA, PHOSPHORYLATION, MAP KINASE
596	1cmk	E	122	434	0	-0.11	0.37		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK3 (E.C.2.7.1.37) ICMK4	
596	1ctp	E	122	434	6.80E-97	0.18	0.48		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP3 (CATALYTIC SUBUNIT) ICTP4	
596	1f3m	C	148	397	6.80E-46	0.35	0.89		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
596	1fgk	B	147	344	5.10E-31	0.14	0.22		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
596	1fgk	B	206	372	7.00E-08	-0.07	0.33		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
596	1fpu	A	192	372	4.20E-06	0.12	0.51		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL, KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
596	1hcl		146	399	1.70E-47	0.26	0.7		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
596	lian		147	349	1.40E-32	0.1	0.65		P38 MAP KINASE; CHAIN: NULL;	MITOSIS, PHOSPHORYLATION SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
596	ljnk		146	346	3.40E-34	0	0.74		C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
596	ljnk		258	351	7.00E-07	-0.12	0.51		C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
596	lkoa		146	400	1.70E-53	0.15	0.66		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
596	lkob	A	141	398	6.80E-54	0.31	0.76		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
596	lp38		147	349	3.40E-36	0.09	0.55		MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
596	lphk		147	397	1.70E-60	0.22	0.88		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE- PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
596	lki	A	143	397	3.40E-41	0.16	0.92		TTIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TTIN, MUSCLE, AUTOINHIBITION
601	lb87	A	17	145	0.0065	0.38	0.86		AMINOGLYCOSIDE N6'- ACETYLTRANSFERASE TYPE 1; CHAIN: A;	TRANSFERASE AAC; AMINOGLYCOSIDE 6'-N- ACETYLTRANSFERASE, ANTIBIOTIC 2 RESISTANCE, ACETYL COENZYME A
602	lega	A	146	171	0.00039	-0.81	0.07		GTP-BINDING PROTEIN ERA; CHAIN: A, B;	HYDROLASE ERA, GTPASE, RNA- BINDING, RAS-LIKE, HYDROLASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
605	1ez3	A	560	699	0.0039	-0.14	0.07		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
605	1pb _w	A	25	192	1.30E-20	0.43	1		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
605	1pb _w	B	25	192	1.30E-20	0.78	1		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
605	1pb _w	B	25	217	2.60E-40	0.77	1		PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
605	1rgp		13	212	1.80E-30			112.2	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE- ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
605	1rgp		16	189	1.80E-30	0.58	1		RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE- ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
605	1tx4	A	15	212	9.10E-48			118.67	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
605	1tx4	A	16	201	1.10E-30	0.54	1		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
605	1tx4	A	16	212	9.10E-48	0.9	1		P50-RHOGAP; CHAIN: A;	COMPLEX(GTPASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									TRANSFORMING PROTEIN RHOA; CHAIN: B;	ACTIVATOR/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOA; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
606	1afi		143	203	0.00026	0.86	1		MERP; CHAIN: NULL;	MERCURY DETOXIFICATION MERCURY TRANSPORT PROTEIN; MERCURY DETOXIFICATION, PERIPLASMIC, HEAVY METAL TRANSPORT, 2 ALPHA-BETA SANDWICH
606	1aw0		143	203	0.0012	0.81	1		MENKES COPPER-TRANSPORTING ATPASE; CHAIN: NULL;	HYDROLASE COPPER-TRANSPORTING ATPASE, COPPER-BINDING DOMAIN, HYDROLASE
606	1ial	A	21	91	1.20E-06	-0.02	0.46		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
606	3bct		16	148	0.00026	0.42	0.96		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
607	1a09	A	150	255	6.50E-41			172.37	C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
607	1a09	A	150	255	6.50E-41	1.07	1		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE); CHAIN: C, D;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)
607	1a81	A	126	255	7.80E-33	0.57	1		SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK, KINASE, SH2 DOMAIN, ITAM

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
607	1a8l	A	151	372	1.30E-46	0.26	0.9		SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, I, L;	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK, KINASE, SH2 DOMAIN, ITAM
607	1apm	E	255	542	1.30E-35			97.15	TRANSFERASE(PHOSPHOTRANSFERASE) \$C\$-AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) IAPM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (S139A\$) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 IAPM 6	
607	1apm	E	282	515	1.30E-35	0.81	1		TRANSFERASE(PHOSPHOTRANSFERASE) \$C\$-AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) IAPM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (S139A\$) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 IAPM 6	
607	1aq1		281	529	1.30E-33	0.34	1		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
607	1b6c	B	241	533	2.60E-74			102.06	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									TYPE I; CHAIN: B, D, F, H;	KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
607	1b6c	B	256	531	2.60E-74	0.51	1		FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
607	1bkl		155	259	2.60E-40	1.13	1		PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN
607	1bkl		155	263	2.60E-40			165.48	PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN
607	1blx	A	269	529	1.20E-34	0.66	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
607	1blx	A	270	538	1.20E-34			99.54	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
607	1cmk	E	282	515	9.10E-35	0.7	1		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
607	1ctp	E	227	542	6.50E-35			99.49	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPIK) 1CTP 3 (CATALYTIC	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
607	1ctp	E	282	515	6.50E-35	0.55	1		SUBUNIT 1CTP 4 TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
607	1f3m	C	272	519	1.30E-42	0.71	1		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D; HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
607	1hcl		273	538	1.30E-37			111.67	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
607	1hcl		281	529	1.30E-37	0.43	1		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
607	1jnk		269	538	1.30E-33	0.6	1		C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
607	1nlo	C	88	149	2.60E-19	0.13	1		C-SRC; CHAIN: C; NLI (MN7-MN2-MN1-PLPPLP); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
607	1p38		269	517	2.60E-32	0.44	1		MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
607	1sha	A	154	256	9.10E-40			165.79	PHOSPHOTRANSFERASE V-SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSINE ISHA 3 RECOGNITION DOMAIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									SH2) (E.C.2.7.1.112) COMPLEX WITH ISHA 4 PHOSHOPEPTIDE A (TYR- VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) ISHA 5	
607	1sha	A	154	256	9.10E-40	0.97	1		PHOSPHOTRANSFERASE V- SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSINE ISHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH ISHA 4 PHOSHOPEPTIDE A (TYR- VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) ISHA 5	
607	1tuc		100	166	1.30E-14	-0.02	0.89		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
607	1tud		75	130	3.90E-09	-0.25	0.01		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
607	2abl		79	255	9.10E-34			121.36	ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
607	2abl		80	255	9.10E-34	0.64	1		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
607	2shp	A	75	425	6.50E-59	-0.13	0.54		SHP-2; CHAIN: A, B;	TYROSINE PHOSPHATASE SYP, SHPTP-2; TYROSINE PHOSPHATASE, INSULIN SIGNALING, SH2 PROTEIN
608	1alh	A	203	284	9.10E-21	-0.13	0.31		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
608	1alh	A	509	590	1.30E-32	0	0.74		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
608	lard		509	537	6.50E-05	-0.34	0.05		OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADR1 (RESIDUES 102 - 130) IARD 3 (AMINO TERMINAL ZINC FINGER DOMAIN) (NMR, 10 STRUCTURES) IARD 4 (ADR1B) IARD 5	FINGER, DNA-BINDING PROTEIN
608	lbbo		485	537	2.60E-16	-0.3	0.17		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 IBBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) IBBO 4	
608	lme y	C	202	283	1.30E-22	0.16	0.87		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	lme y	C	230	311	6.50E-33	0.32	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	lme y	C	259	339	1.20E-42	0.89	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	lme y	C	286	367	5.20E-44	0.67	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	lme y	C	314	395	9.10E-47	0.62	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
608	1mey	C	314	396	9.10E-47			102.94	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	1mey	C	342	423	7.80E-46	0.74	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	1mey	C	370	451	1.30E-45	0.53	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	1mey	C	398	479	1.30E-40	0.33	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	1mey	C	426	505	2.60E-34	0.05	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	1mey	C	454	589	3.90E-32	-0.08	0.22		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	1mey	C	536	617	3.90E-42	0.2	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	1mey	C	564	645	3.90E-46	0.29	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
608	1mey	C	592	673	2.60E-46	0.33	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	1mey	C	620	702	2.60E-45	0.6	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
608	1sp1		509	537	7.80E-05	-0.29	0.01		SPIF3; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI
608	1sp2		509	537	9.10E-05	-0.23	0.13		SPIF2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI
608	1tf6	A	342	505	2.60E-71			109.61	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
608	1tfi		480	520	0.0091	-0.22	0.24		TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII (TFIIS, NUCLEIC-ACID 1TFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) 1TFI 4	
608	1ubd	C	165	311	7.80E-29	-0.34	0.03		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
608	1ubd	C	229	340	6.50E-43	0.26	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
608	1ubd	C	263	368	7.80E-52	0.55	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
608	1ubd	C	284	395	1.30E-53	0.58	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
608	1ubd	C	341	451	5.20E-53	0.26	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
608	1ubd	C	374	479	9.10E-51	0.34	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
608	1ubd	C	424	589	2.60E-39	-0.28	0.34		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
608	1ubd	C	508	618	5.20E-45	-0.04	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
608	1ubd	C	564	674	5.20E-56	-0.07	1		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
608	1ubd	C	590	701	1.30E-54	0.06	1		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
608	2adr		455	509	2.60E-18	-0.15	0.41		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
608	2drp	A	479	530	1.30E-15	0.11	0.06		COMPLEX (TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
608	2drp	A	505	563	6.50E-18	0.28	0.23		COMPLEX (TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
608	2gli	A	230	369	9.10E-58	0.1	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
608	2gli	A	259	397	1.00E-65	0.45	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
608	2gli	A	314	480	1.30E-67	0.32	1		ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
608	2gli	A	398	619	1.30E-56	0	0.37		CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
608	2gli	A	536	675	1.30E-64	0.3	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
608	2gli	A	564	701	2.60E-70	0.16	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
608	2gli	A	564	703	2.60E-70			92.71	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
609	1am4	D	6	165	2.60E-20	0.46	1		P50-RHO GAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING) COMPLEX (GTPASE-ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
609	1byu	B	1	192	3.90E-24			55.55	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
609	1byu	B	6	181	3.90E-24	0.15	0.66		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
609	1cxz	A	1	187	1.30E-20			61.64	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
609	1cxz	A	6	170	1.30E-20	0.19	1		HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
609	1ds6	A	6	172	2.60E-20	0.14	1		RAS-RELATED C3 BOTULINUM TOXIN	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI, BETA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SANDWICH, PROTEIN-PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN
609	1e0s	A	6	168	1.20E-22	0.12	0.57		ADP-RIBOSYLATION FACTOR 6; CHAIN: A;	G PROTEIN G PROTEIN, RAS, ARF, ARF6, MEMBRANE TRAFFIC
609	1hur	A	1	172	7.80E-23			55.9	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16
609	1hur	A	6	168	7.80E-23	-0.12	0.55		HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16
609	1ibr	A	3	174	3.90E-23			71.05	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
609	1ibr	A	6	173	3.90E-23	0.04	0.99		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
609	1mh1		2	189	3.90E-21			52.65	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
609	1mh1		6	171	3.90E-21	0.36	1		RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
609	1rrp	C	3	187	9.10E-24			77.78	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
609	1rrp	C	6	180	9.10E-24	-0.02	0.6		RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
609	1rx4	B	2	185	2.60E-20			54.35	P50-RHO GAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHO GAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
609	1rx4	B	5	165	2.60E-20	0.37	1		P50-RHO GAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
										RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
612	1blx	A	370	691	2.60E-52			129.83	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
612	1hcl		371	687	7.80E-50			118.75	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
628	1ayz	A	167	337	1.00E-15			54.69	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
628	1qcq	A	168	335	2.60E-17			54.87	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
628	2aak		167	333	2.60E-14			59.33	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
631	1aj4		317	468	5.20E-06			70.38	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
631	1aur	B	320	476	7.80E-21			78.45	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
631	1iku		311	491	5.20E-20			67.12	RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
631	1tcf		320	465	9.10E-17			68.38	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
631	1tnx		320	463	1.20E-16			67.26	TROPONIN C; ITNX 4	CALCIUM-BINDING PROTEIN EF-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: NULL; ITNX 5	HAND ITNX 14
646	lbe4	A	1	115	3.60E-53			105.78	NUCLEOSIDE DIPHOSPHATE TRANSFERASE; CHAIN: A, B, C;	PHOSPHOTRANSFERASE PHOSPHOTRANSFERASE
646	lnsq	A	1	115	3.60E-50			104.27	PHOSPHOTRANSFERASE NUCLEOSIDE DIPHOSPHATE KINASE (E.C.2.7.4.6) INSQ 3	
646	lnue	A	1	116	9.00E-53			105.45	NUCLEOSIDE DIPHOSPHATE KINASE; INUE 4 CHAIN: A, B, C, D, E, F; INUE 5	PHOSPHOTRANSFERASE NUCLEOSIDE TRIPHOSPHATE, NUCLEOSIDE DIPHOSPHATE INUE 10
658	lam4	D	88	263	3.60E-56	0.31	0.55		P50-RHOGAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING) COMPLEX (GTPASE-ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
658	lcly	A	86	264	5.40E-56	0.17	0		RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
658	lcc0	A	89	271	9.00E-62	0.24	0.65		TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN
658	lctq	A	86	265	1.80E-59	0.23	0.36		TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
658	lcz	A	89	264	9.00E-62	0.39	0.93		HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
658	lds6	A	88	267	1.40E-62	0.05	0.54		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWICH, PROTEIN-PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
658	1hur	A	75	266	7.20E-11			54.59	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7 RAC1; CHAIN: NULL;	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16
658	1mh 1		88	267	1.30E-63	0.19	0.45			GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
658	1x4	B	89	263	1.80E-58	0.31	0.82		P50-RHOA; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOA; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
658	2nig	A	88	270	7.20E-60	-0.01	0.4		GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
658	3rab	A	86	265	1.10E-54	0.11	0.47		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
659	1bor		16	59	9.00E-06	-0.73	0.25		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2
659	1chc		16	60	9.00E-15	0.24	0.98		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	TRANSCRIPTION REGULATION
659	1fbv	A	18	66	1.80E-10	0.25	0.9		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
659	1g25	A	18	72	1.30E-05	-0.44	0.09		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)
661	1pir		172	218	0.002	-0.75	0.21		PCRA; CHAIN: NULL;	HELICASE DNA REPAIR, DNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
661	1qhg	B	172	202	0.0045	-0.84	0.28		PCRA (SUBUNIT); CHAIN: A; PCRA (SUBUNIT); CHAIN: B; PCRA (SUBUNIT); CHAIN: C; PCRA (SUBUNIT); CHAIN: D;	REPLICATION, SOS RESPONSE, HELICASE, 2 ATP-BINDING, DNA- BINDING
661	luua	A	172	238	0.00011	-0.67	0.69		ATP-DEPENDENT DNA HELICASE REP; CHAIN: A, B; DNA CHAIN: C;	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, ATP-2 BINDING, DNA- BINDING
661	2pjr	A	172	236	9.00E-06	-0.31	0.88		HELICASE PCRA; CHAIN: A; F; HELICASE PCRA; CHAIN: B, G; DNA (5'- D(*Tp*Tp*Tp*Tp*T)-3'); CHAIN: C, D; DNA (5'- D(*Gp*C)-3'); CHAIN: H; DNA (5'-D(*Ap* Cp*Tp*Gp*C)-3'); CHAIN: I;	COMPLEX (HELICASE/DNA) COMPLEX (HELICASE/DNA), HELICASE, DNA UNWINDING HYDROLASE/DNA ATP-DEPENDENT HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX
663	1eo0	A	1	64	1.00E-18	-0.43	0.24		TRANSCRIPTION ELONGATION FACTOR S-II; CHAIN: A;	TRANSCRIPTION HELIX-BUNDLE
663	1eo0	A	4	64	3.60E-12	0.45	0.18		TRANSCRIPTION ELONGATION FACTOR S-II; CHAIN: A;	TRANSCRIPTION HELIX-BUNDLE
663	1tff		283	332	1.30E-22	0.45	1		TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII (TFIS, NUCLEIC-ACID ITFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) ITFI 4	
663	1tff		283	332	3.90E-24			84.88	TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII (TFIS, NUCLEIC-ACID ITFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) ITFI 4	
663	1tff		283	332	3.90E-24	0.45	1		TRANSCRIPTION REGULATION	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									TRANSCRIPTIONAL ELONGATION FACTOR SII (TFIIS, NUCLEIC-ACID ITFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) ITFI 4	
664	1di2	A	388	452	1.60E-13	0.06	0.99		DOUBLE STRANDED RNA BINDING PROTEIN A; CHAIN: A, B; RNA (5'-R(*GP*GP*CP*GP*CP*GP*CP *GP*CP*C)-3'); CHAIN: C, D, E, G;	RNA BINDING PROTEIN/RNA XLRBPA; PROTEIN-RNA COMPLEX, DOUBLE STRANDED RNA, PROTEIN-RNA 2 INTERACTIONS, RNA-BINDING PROTEIN, RNA BINDING PROTEIN/RNA
664	1di2	A	390	451	1.30E-14	0.45	0.42		DOUBLE STRANDED RNA BINDING PROTEIN A; CHAIN: A, B; RNA (5'-R(*GP*GP*CP*GP*CP*GP*CP *GP*CP*C)-3'); CHAIN: C, D, E, G;	RNA BINDING PROTEIN/RNA XLRBPA; PROTEIN-RNA COMPLEX, DOUBLE STRANDED RNA, PROTEIN-RNA 2 INTERACTIONS, RNA-BINDING PROTEIN, RNA BINDING PROTEIN/RNA
664	1di2	A	512	574	2.60E-16	0.11	0.99		DOUBLE STRANDED RNA BINDING PROTEIN A; CHAIN: A, B; RNA (5'-R(*GP*GP*CP*GP*CP*GP*CP *GP*CP*C)-3'); CHAIN: C, D, E, G;	RNA BINDING PROTEIN/RNA XLRBPA; PROTEIN-RNA COMPLEX, DOUBLE STRANDED RNA, PROTEIN-RNA 2 INTERACTIONS, RNA-BINDING PROTEIN, RNA BINDING PROTEIN/RNA
664	1di2	A	514	558	1.80E-09	-0.16	0.39		DOUBLE STRANDED RNA BINDING PROTEIN A; CHAIN: A, B; RNA (5'-R(*GP*GP*CP*GP*CP*GP*CP *GP*CP*C)-3'); CHAIN: C, D, E, G;	RNA BINDING PROTEIN/RNA XLRBPA; PROTEIN-RNA COMPLEX, DOUBLE STRANDED RNA, PROTEIN-RNA 2 INTERACTIONS, RNA-BINDING PROTEIN, RNA BINDING PROTEIN/RNA
664	1di2	B	388	452	1.60E-07	0.06	0.7		DOUBLE STRANDED RNA BINDING PROTEIN A; CHAIN: A, B; RNA (5'-R(*GP*GP*CP*GP*CP*GP*CP *GP*CP*C)-3'); CHAIN: C, D, E, G;	RNA BINDING PROTEIN/RNA XLRBPA; PROTEIN-RNA COMPLEX, DOUBLE STRANDED RNA, PROTEIN-RNA 2 INTERACTIONS, RNA-BINDING PROTEIN, RNA BINDING PROTEIN/RNA
664	1ekz	A	380	454	1.80E-14	-0.12	0.31		MATERNAL EFFECT PROTEIN (STAUFEN); CHAIN: A; STAUFEN DOUBBLE-STRANDED RNA BINDING DOMAIN; CHAIN:	CELL CYCLE/RNA DSRBDIII; NMR STRUCTURE, PROTEIN/RNA, PROTEIN DSRBD, DROSOPHILA. RNA 2 HAIRPIN

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664	1ekz	A	384	451	5.20E-15	-0.06	0.69		B; MATERNAL EFFECT PROTEIN (STAUFEN); CHAIN: A; STAUFEN DOUBLE-STRANDED RNA BINDING DOMAIN; CHAIN: B;	CELL CYCLE/RNA DSRBDIII; NMR STRUCTURE, PROTEIN/RNA, PROTEIN DSRBD, DROSOPHILA, RNA 2 HAIRPIN
664	1ekz	A	509	557	5.40E-05	0.04	0.39		B; MATERNAL EFFECT PROTEIN (STAUFEN); CHAIN: A; STAUFEN DOUBLE-STRANDED RNA BINDING DOMAIN; CHAIN: B;	CELL CYCLE/RNA DSRBDIII; NMR STRUCTURE, PROTEIN/RNA, PROTEIN DSRBD, DROSOPHILA, RNA 2 HAIRPIN
664	1ekz	A	511	574	1.30E-19	0.75	1		B; MATERNAL EFFECT PROTEIN (STAUFEN); CHAIN: A; STAUFEN DOUBLE-STRANDED RNA BINDING DOMAIN; CHAIN: B;	CELL CYCLE/RNA DSRBDIII; NMR STRUCTURE, PROTEIN/RNA, PROTEIN DSRBD, DROSOPHILA, RNA 2 HAIRPIN
664	1qu6	A	375	469	1.10E-15	-0.17	0.06		PROTEIN KINASE PKR; CHAIN: A;	TRANSFERASE DSRNA-BINDING DOMAIN, NMR, PKR, SOLUTION STRUCTURE, PROTEIN 2 KINASE, TRANSFERASE
664	1qu6	A	518	558	7.20E-08	-0.05	0.09		PROTEIN KINASE PKR; CHAIN: A;	TRANSFERASE DSRNA-BINDING DOMAIN, NMR, PKR, SOLUTION STRUCTURE, PROTEIN 2 KINASE, TRANSFERASE
664	1stu		388	454	3.60E-13	0.23	0.07		MATERNAL EFFECT PROTEIN STAUFEN; 1STU 4	DOUBLE STRANDED RNA BINDING DOMAIN STAUFEN 1STU 13
664	1stu		512	575	3.90E-18	0.19	1		MATERNAL EFFECT PROTEIN STAUFEN; 1STU 4	DOUBLE STRANDED RNA BINDING DOMAIN STAUFEN 1STU 13
664	1stu		514	557	0.0009	-0.24	0.11		MATERNAL EFFECT PROTEIN STAUFEN; 1STU 4	DOUBLE STRANDED RNA BINDING DOMAIN STAUFEN 1STU 13
665	1b7f	A	1	84	1.30E-10	0.48	0.92		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*Gp*UP*UP*GP*UP*UP*U P*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
665	1cvj	B	10	88	9.10E-11	1.05	1		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C,	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM,

SEQ ID NO;	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP)-3'); CHAIN: M, N, O, P, Q, R, S, T;	PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
665	1cvj	H	10	88	7.80E-11	1.03	1		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
665	1d9a	A	9	88	1.30E-11	0.84	0.99		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
665	1fj7	A	8	89	2.60E-11	0.56	0.64		NUCLEOLIN RBD1; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
665	1sxl		6	88	1.30E-11	0.72	0.8		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	
665	2sxl		9	88	2.60E-11	1.18	1		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
665	2u2f	A	9	88	7.80E-11	0.89	1		SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN COMPLEX
665	2upl	A	5	88	6.50E-11	0.87	1		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRAINED TELOMETRIC DNA; CHAIN: B;	(RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1
666	1crz	A	126	269	0.0013	0.18	0.04		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
666	1crz	A	77	217	3.90E-06	0.21	0.39		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
666	1ej	A	1	315	1.80E-59	0.2	0.84		TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	ALPHA/BETA FOLD TRANSCRIPTION INHIBITOR BETA-PROPELLER
666	1ej	A	30	373	3.60E-69	0.24	0.69		TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
666	1got	B	1	271	7.20E-73	0.59	1		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
666	1got	B	118	420	1.10E-57	0.27	-0.02		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
666	1got	B	29	372	1.10E-57			91.76	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
666	1got	B	71	370	5.40E-56	0.56	0.8		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
669	1d0s	A	9	194	7.80E-14	0.52	-0.18		NICOTINATE	TRANSFERASE DINUCLEOTIDE-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									MONONUCLEOTIDE:5,6-CHAIN: A;	BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
671	1eo0	A	1	64	1.00E-18	-0.43	0.24		TRANSCRIPTION ELONGATION FACTOR S-II; CHAIN: A;	TRANSCRIPTION HELIX-BUNDLE
671	1eo0	A	4	60	1.10E-06	-0.03	0.21		TRANSCRIPTION ELONGATION FACTOR S-II; CHAIN: A;	TRANSCRIPTION HELIX-BUNDLE
671	1tff		211	257	1.80E-21	0.24	1		TRANSCRIPTION REGULATION ELONGATION FACTOR SII (TFIIS, NUCLEIC-ACID ITFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) ITFI 4	
671	1tff		212	257	1.30E-21			75.24	TRANSCRIPTION REGULATION ELONGATION FACTOR SII (TFIIS, NUCLEIC-ACID ITFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) ITFI 4	
671	1tff		212	257	1.30E-21	0.26	1		TRANSCRIPTION REGULATION ELONGATION FACTOR SII (TFIIS, NUCLEIC-ACID ITFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) ITFI 4	
672	1bor		300	342	1.40E-06	-0.65	0.01		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2
672	1chc		302	352	1.80E-13	-0.48	0.6		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	TRANSCRIPTION REGULATION
672	1fbv	A	277	351	9.10E-11	-0.62	0.45		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
672	1fbv	A	301	349	3.60E-13	-0.4	0.55		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
672	1qbh	A	227	270	0.0027	-0.73	0.37		INHIBITOR OF APOPTOSIS PROTEIN (2MIHB/C-IAP-1); CHAIN: A;	APOPTOSIS INHIBITOR OF APOPTOSIS (IAP), NMR STRUCTURE, BACULOVIRAL 2 IAP REPEAT (BIR), ZINC BINDING DOMAIN
672	1rmd		267	344	2.60E-09	0.34	0.8		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
672	1rmd		302	342	7.20E-09	-0.11	0.84		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
673	1amu	A	24	576	0			158.05	GRAMICIDIN SYNTHETASE 1; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING
673	1amu	A	39	571	0	0.6	1		GRAMICIDIN SYNTHETASE 1; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING
673	1lci		22	574	3.60E-93			173.59	LUCIFERASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
673	1lci		36	571	3.60E-93	0.77	1		LUCIFERASE; CHAIN: NULL;	OXIDOREDUCTASE, OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE
675	1bor		144	192	0.0031	0.21	0.01		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2
675	1bor		144	192	0.00054	0.21	0.01		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2
676	1bor		144	192	0.0031	0.21	0.01		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2
676	1bor		144	192	0.00054	0.21	0.01		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2
679	1msp	A	34	125	7.80E-06	-0.05	0.07		MAJOR SPERM PROTEIN; CHAIN: A, B;	CELL MOTILITY PROTEIN MSP; CYTOSKELETAL PROTEIN, SPERM, CELL MOTILITY PROTEIN
680	1msp	A	34	125	7.80E-06	-0.05	0.07		MAJOR SPERM PROTEIN; CHAIN: A, B;	CELL MOTILITY PROTEIN MSP; CYTOSKELETAL PROTEIN, SPERM, CELL MOTILITY PROTEIN
681	1ez3	A	165	286	7.80E-09	0.12	-0.19		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
682	1b3u	A	1	377	1.10E-51	0.16	-0.02		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
682	1ibr	B	22	119	5.40E-07	0.02	0.06		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
682	1qbk	B	2	400	3.60E-37	0.11	0.07		CHAIN: B, D; KARYOPHERIN BETA2; CHAIN: B, RAN; CHAIN: C;	TRANSPORT RECEPTOR NUCLEAR TRANSPORT PROTEIN COMPLEX HEAT REPEATS, NUCLEAR TRANSPORT PROTEIN COMPLEX
682	3bet		32	363	1.30E-07	-0.18	0.09		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
683	1e3h	A	1	273	7.20E-58	0.55	1		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP 2 DIPHOSPHOTRANSFERASE, RNA PROCESSING, RNA DEGRADATION
683	1e3p	A	1	273	7.20E-58	0.62	1		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP DIPHOSPHOTRANSFERASE, 2 RNA PROCESSING, RNA DEGRADATION
684	1e5d	A	68	191	3.60E-13	0.03	-0.06		RUBREDOXIN-OXYGEN OXIDOREDUCTASE; CHAIN: A, B	OXIDOREDUCTASE OXIDOREDUCTASE, OXYGENREDUCTASE, DIIRON- CENTRE, 2 FLAVOPROTEINS, LACTAMASE-FOLD
684	1sml	A	34	198	1.30E-18	0.29	0.04		PENICILLINASE; CHAIN: A;	HYDROLASE METALLO-BETA- LACTAMASE, ANTIBIOTIC RESISTANCE, BINUCLEAR 2 ZINC, HYDROLASE
684	1sml	A	498	558	0.00052	-0.22	0.09		PENICILLINASE; CHAIN: A;	HYDROLASE METALLO-BETA- LACTAMASE, ANTIBIOTIC RESISTANCE, BINUCLEAR 2 ZINC, HYDROLASE
684	2bc2	A	45	187	3.60E-10	0.05	-0.05		METALLO BETA- LACTAMASE II; CHAIN: A, B;	HYDROLASE HYDROLASE, BETA- LACTAMASE, ANTIBIOTIC, METALLOENZYME
686	1quq	A	28	181	3.60E-38	0.01	0.23		REPLICATION PROTEIN A 32	DNA-BINDING PROTEIN RPA, OB-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									KD SUBUNIT; CHAIN: A, C; REPLICATION PROTEIN A 14 KD SUBUNIT; CHAIN: B, D;	FOLD, SSDNA-BINDING, DNA-BINDING PROTEIN
690	1dby	A	62	147	3.60E-13	-0.28	0.11		CHLOROPLAST THIOREDOXIN M CH2; CHAIN: A;	OXIDOREDUCTASE THIOREDOXIN M, THIOREDOXIN CH2, CHLOROPLASTIC THIOREDOXIN
690	1erv		60	142	3.60E-07	0.08	0.09		THIOREDOXIN; CHAIN: NULL;	OXIDOREDUCTASE DIMER, THIOREDOXIN, X-RAY CRYSTALLOGRAPHY, OXIDOREDUCTASE
690	1fb6	A	60	143	3.60E-11	-0.31	0.01		THIOREDOXIN M; CHAIN: A; B;	ELECTRON TRANSPORT ELECTRON TRANSPORT
690	1qk8	A	70	127	5.40E-07	-0.87	0.18		TRYPAREDOXIN-I; CHAIN: A;	TRYPAREDOXIN TRYX-J; TRYPAREDOXIN, CRITHIDIA FASCICULATA, THIOREDOXIN, 2 TRYPANOSOME, ANOMALOUS DISPERSION, OXIDATIVE STRESS, 3 OXIDOREDUCTASE
690	1qk8	A	75	181	1.30E-12	0.32	0.34		TRYPAREDOXIN-I; CHAIN: A;	TRYPAREDOXIN TRYX-J; TRYPAREDOXIN, CRITHIDIA FASCICULATA, THIOREDOXIN, 2 TRYPANOSOME, ANOMALOUS DISPERSION, OXIDATIVE STRESS, 3 OXIDOREDUCTASE
690	1qm _v	A	48	233	5.40E-40	0.06	-0.14		HUMAN THIOREDOXIN PEROXIDASE-B; CHAIN: A, B, C, D, E, F, G, H, I, J;	PEROXIDASE 2-CYS PEROXIREDOXIN, CALPROMOTIN PEROXIDASE, PEROXIREDOXIN, SULPHINIC ACID, THIOREDOXIN
690	1qq2	A	48	210	1.60E-40	0.1	0.09		THIOREDOXIN PEROXIDASE 2; CHAIN: A, B;	OXIDOREDUCTASE HEME-BINDING PROTEIN 23 KD, HBP23; THIOREDOXIN FOLD, OXIDOREDUCTASE
690	1qu _w	A	78	187	1.30E-06	-0.66	0.11		THIOREDOXIN; CHAIN: A;	ELECTRON TRANSPORT ALPHA/BETA OPEN-TWISTED PROTEIN, THIOL-DISULFIDE
690	1v7p	B	62	150	1.60E-12	-0.36	0.03		DNA POLYMERASE; CHAIN: A; THIOREDOXIN; CHAIN: B; DNA; CHAIN: P, T;	T7 DNA POLYMERASE, DNA REPLICATION, NUCLEOTIDYL 2 TRANSFERASE, SEQUENCING, THIOREDOXIN, PROCESSIVITY FACTOR, 3 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
690	2trx	A	62	150	1.60E-12	-0.1	0.04		ELECTRON TRANSPORT THIOREDOXIN 2TRXA 2 2TRXA 3	(HYDROLASE/ELECTRON TRANSPORT/DNA)
691	1chc		318	363	7.20E-13	-0.33	0.48		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
691	1fbv	A	298	363	1.20E-10	-0.58	0.21		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
691	1fbv	A	319	368	1.80E-06	-0.74	0.21		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
691	1rmd		297	363	1.00E-13	-0.07	0.94		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
691	1rmd		319	368	5.40E-06	-0.24	0.49		RAG1; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
693	1erj	A	4	307	5.40E-42	0.66	0.11		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
693	1erj	A	71	369	9.00E-51	0.52	0.29		TRANSCRIPTIONAL	TRANSCRIPTION INHIBITOR BETA-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
693	1got	B	28	376	3.60E-57			70.14	REPRESSOR TUP1; CHAIN: A, B, C; GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	PROPELLER
693	1got	B	39	370	3.60E-57	0.39	0.16		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
693	1got	B	5	304	1.40E-36	0.26	-0.17		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
694	1crz	A	133	377	9.00E-08	0.2	0.29		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
694	1erj	A	108	416	5.40E-78	0.12	0.94		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
694	1erj	A	18	313	1.80E-65	0.46	1		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
694	1erj	A	195	442	9.00E-57	0.01	0.99		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
694	1erj	A	5	224	1.40E-52	0.27	0.16		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A;	TRANSCRIPTION INHIBITOR BETA-PROPELLER

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
694	1got	B	103	393	5.40E-64	0.54	1		B, C; GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
694	1got	B	12	353	7.20E-81			105.8	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
694	1got	B	190	443	3.60E-50	0.26	0.21		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
694	1got	B	4	267	1.80E-53	0.36	0.22		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
694	1got	B	56	353	7.20E-81	0.69	1		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
697	1alh	A	200	282	1.30E-31			84.99	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
697	1alh	A	228	309	3.60E-27	0.18	1		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
697	1alh	A	228	337	1.30E-31	-0.13	0.03		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
697	1alh	A	341	421	7.20E-30	0.03	0.81		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
697	1alh	A	397	480	1.80E-28	0	0.69		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
697	1alh	A	40	98	5.40E-10	0.13	-0.17		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
697	1alh	A	484	554	5.40E-28	0.14	0.69		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
697	1alh	A	74	154	3.60E-26	-0.1	0.39		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
697	1bbo		514	564	6.50E-11	-0.35	0.09		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 111 BBBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO 4	
697	1me	C	101	168	1.80E-36	-0.09	0.45		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
	y								CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1me y	C	102	224	1.30E-16	-0.26	0.16		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1me y	C	156	252	9.00E-35	-0.15	0.8		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1me y	C	199	280	5.40E-47	0.31	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1me y	C	199	281	5.40E-47			97.32	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1me y	C	227	309	3.60E-46	0.27	0.96		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1me y	C	227	337	1.30E-33	-0.23	0.22		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1me y	C	283	365	3.60E-47	0.21	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1me y	C	312	393	1.40E-49	0.41	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	C	340	422	1.30E-48	0.09	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	C	368	451	1.80E-48	0	0.88		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	C	368	508	1.30E-21	-0.68	0.04		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	C	396	480	3.60E-47	0.03	0.62		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	C	42	126	1.60E-35	-0.13	0		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	C	425	508	3.60E-48	0.22	0.86		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	C	455	536	3.60E-50	0.31	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	C	483	557	1.10E-44	0.18	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
697	1mey	C	73	154	1.80E-43	-0.2	0.58		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	G	509	536	5.40E-13	0.53	0.94		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1mey	G	71	98	1.10E-09	0.3	-0.13		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
697	1tf3	A	341	417	1.10E-19	-0.1	0.4		TRANSCRIPTION FACTOR IIIA; CHAIN: A, 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
697	1tf6	A	199	366	2.60E-50			107.54	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
697	1tf6	A	200	346	3.60E-37	-0.08	0.92		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
697	1tf6	A	313	461	3.60E-34	-0.02	0.75		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
697	1tf6	A	341	489	5.40E-36	-0.13	0.23		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
697	1tf6	A	426	558	1.80E-30	-0.02	0.72		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
697	1tf6	A	74	233	1.80E-27	-0.39	0.01		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
697	1ubd	C	104	224	1.80E-20	-0.35	0.69		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	204	338	1.30E-39	-0.29	0.51		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	235	337	1.30E-31	-0.18	0.95		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	260	393	1.30E-32	-0.36	0.28		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	263	365	1.80E-33	-0.3	0.7		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	320	422	9.00E-35	-0.03	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	345	450	2.60E-28	-0.11	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	404	508	3.60E-32	0	0.51		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	427	537	1.80E-34			83.84	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
697	1ubd	C	433	536	1.80E-34	0.06	0.88		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	463	558	3.60E-32	-0.05	0.46		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	69	154	1.30E-26	-0.25	0.35		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	1ubd	C	78	253	1.30E-18	-0.45	0.07		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
697	2adr		512	560	2.60E-14	-0.15	0.31		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
697	2dtp	A	508	564	1.30E-15	0.26	-0.12		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
697	2gli	A	101	279	7.20E-26	-0.08	0.45		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
697	2gli	A	102	282	6.50E-40	-0.17	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	198	308	7.20E-28	0.14	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	200	394	5.20E-48	-0.24	0.25		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	235	367	1.80E-32	0.06	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	255	397	5.20E-48			89.2	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	292	422	5.40E-35	-0.02	0.78		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	320	449	3.60E-34	0.04	0.86		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	404	535	5.40E-33	0.2	0.92		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	433	558	1.60E-31	0.02	0.22		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	66	153	1.10E-24	-0.05	0.03		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
697	2gli	A	77	253	3.90E-30	-0.45	0.13		ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
698	1edh	A	101	302	7.20E-32	-0.1	0.63		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
698	1edh	A	74	300	7.20E-32			62.4	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
698	1ncj	A	6	178	1.40E-34	0.04	-0.12		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
698	1ncj	A	70	302	1.80E-32			64.18	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
698	1ncj	A	74	302	1.80E-32	-0.03	0.16		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
698	1suh		23	62	1.30E-06	-0.22	0.04		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
698	1suh		74	182	1.30E-08	-0.08	0.01		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
701	1a7j		128	281	1.30E-13	0.17	0.6		PHOSPHORIBULOKINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, KINASE, CALVIN CYCLE
701	1a7j		95	366	1.30E-13			66.9	PHOSPHORIBULOKINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, KINASE, CALVIN CYCLE
701	1bd3	D	306	532	2.60E-73			191.89	URACIL PHOSPHORIBOSYLTRANSFERASE; CHAIN: D, C, B, A;	TRANSFERASE UPRTASE; TRANSFERASE, GLYCOSYLTRANSFERASE, UPRTASE
701	1bd3	D	322	532	3.60E-44	0.84	1		URACIL PHOSPHORIBOSYLTRANSFERASE; CHAIN: D, C, B, A;	TRANSFERASE UPRTASE; TRANSFERASE, GLYCOSYLTRANSFERASE, UPRTASE
701	1bd3	D	324	532	2.60E-73	0.76	1		URACIL PHOSPHORIBOSYLTRANSFERASE; CHAIN: D, C, B, A;	TRANSFERASE UPRTASE; TRANSFERASE, GLYCOSYLTRANSFERASE, UPRTASE
701	1esm	A	75	294	1.80E-35	0.43	0.96		PANTOTHENATE KINASE;	TRANSFERASE PANK; PROTEIN-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
701	1esm	A	91	303	6.50E-67	0.55	0.99		CHAIN: A, B, C, D; PANTOTHENATE KINASE; CHAIN: A, B, C, D;	INHIBITOR COMPLEX TRANSFERASE PANK; PROTEIN-INHIBITOR COMPLEX
701	1ukz		94	302	1.20E-15	0.19	0.54		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3	
701	1zin		105	302	0.0078	-0.33	0.21		ADENYLATE KINASE; CHAIN: NULL;	PHOSPHOTRANSFERASE ADK; PHOSPHOTRANSFERASE, ZINC FINGER
701	3tmk	C	96	303	1.30E-23	-0.38	0.03		THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	KINASE KINASE, PHOSPHOTRANSFERASE
702	1bq0		8	84	1.30E-31			54.61	DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
702	1bq0		9	84	1.30E-31	0.52	0.52		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
702	1cvj	A	182	255	3.60E-14	0.07	0.69		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
702	1cvj	F	182	259	1.80E-12	0.13	0.46		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
702	1cvj	H	182	259	1.80E-12	0.03	0.46		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
702	1d8z	A	185	251	1.80E-12	0.15	0.93		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
702	1ez3	A	77	186	1.30E-09	0.14	-0.13		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
702	1ha1		182	249	1.30E-22	0.33	0.19		HNRNP A1; CHAIN: NULL;	KDA PROTEIN, P35A, THREE HELIX BUNDLE
702	1hd1	A	182	249	5.40E-16	0.12	0.51		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2
702	1hdj		11	78	2.60E-19	0.57	1		HUMAN HSP40; CHAIN: NULL;	RIBONUCLEOPROTEIN RNA BINDING PROTEIN RNA-BINDING DOMAIN
702	1hdj		8	84	1.80E-28			56.45	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
702	1hdj		8	84	1.80E-28	0.01	0.47		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
702	2mss	A	182	249	7.20E-17	0.42	0.18		MUSASHI1; CHAIN: A;	MOLECULAR CHAPERONE HDJ-1; RNA BINDING PROTEIN RNA-BINDING DOMAIN
702	2up1	A	165	255	5.40E-26	0.16	0		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
702	2up1	A	182	259	1.30E-18	-0.11	0.05		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
705	1ez3	A	468	575	6.50E-06	0.15	0.11		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
706	1awc	B	137	292	1.80E-36			63.45	GA BINDING PROTEIN	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
									ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
706	lawc	B	169	273	1.30E-30	0.84	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
706	lawc	B	175	323	1.80E-36	0.49	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
706	lawc	B	209	351	7.20E-33	0.51	0.86		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
706	1bd8		144	298	3.60E-31			62.42	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
706	1bd8		145	293	3.60E-31	0.85	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
706	1bd8		178	320	9.00E-31	0.72	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
706	1bd8		57	224	3.60E-27	0.03	-0.14		P19INK4D CDK4/6	TUMOR SUPPRESSOR TUMOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
706	1blx	B	144	297	1.10E-30			63.41	INHIBITOR; CHAIN: NULL;	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
706	1blx	B	145	293	1.80E-30	0.71	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
706	1blx	B	178	315	1.10E-30	0.65	0.96		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
706	1blx	B	57	224	3.60E-26	0.24	-0.13		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
706	1bu9	A	134	302	9.00E-34			74.38	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
706	1bu9	A	175	329	9.00E-34	0.61	0.95		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
706	1d9s	A	171	273	1.30E-28	0.55	1		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
706	1ihb	A	138	296	5.40E-33			68.42	CYCLIN-DEPENDENT KINASE 6 INHIBITOR;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A, B;	INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
706	lihb	A	175	328	5.40E-33	0.88	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
706	likn	D	82	290	7.20E-41	0.26	0.96		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
706	likn	D	95	307	7.20E-41			74.07	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
706	lmy _o		169	288	2.60E-32			60.99	MYOTROPHIN; CHAIN:	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
706	lmy _o		172	287	2.60E-32	0.32	1		MYOTROPHIN; CHAIN:	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
706	lnfi	E	12	208	1.10E-36	0	-0.06		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
706	lnfi	E	136	310	5.40E-36	0.69	1		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
706	lnfi	E	169	341	1.80E-34	0.55	0.46		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
706	lnfi	E	204	414	3.60E-27	0.18	0.18		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
706	lnfi	E	81	290	3.60E-41	0.26	0.98		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
706	lnfi	E	95	303	3.60E-41			71.81	NF-KAPPA-B P65; CHAIN: A;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
706	1ycs	B	170	362	1.80E-25			75.09	C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F; P53; CHAIN: A; 53BP2; CHAIN: B;	REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
709	1a8y		19	336	5.40E-42			87.98	CALSEQUESTIN; CHAIN: NULL	CALCIUM-BINDING PROTEIN CALSEQUESTIN, CALCIUM-BINDING PROTEIN, SARCOPLASMIC 2 RETICULUM, RABBIT SKELETAL MUSCLE
709	1a8y		20	332	5.40E-42	0.15	0.96		CALSEQUESTIN; CHAIN: NULL	CALCIUM-BINDING PROTEIN CALSEQUESTIN, CALCIUM-BINDING PROTEIN, SARCOPLASMIC 2 RETICULUM, RABBIT SKELETAL MUSCLE
709	1bjx		133	239	1.60E-13	-0.03	0.07		PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE CENTER, ISOMERASE, 2
709	1dby	A	23	131	5.40E-24			52.47	CHLOROPLAST THIOREDOXIN M CH2; CHAIN: A;	ENDOPASMIC RETICULUM OXIDOREDUCTASE THIOREDOXIN M, THIOREDOXIN CH2, CHLOROPLASTIC THIOREDOXIN
709	1dby	A	30	131	5.40E-24	0.3	0.95		CHLOROPLAST THIOREDOXIN M CH2; CHAIN: A;	OXIDOREDUCTASE THIOREDOXIN M, THIOREDOXIN CH2, CHLOROPLASTIC THIOREDOXIN
709	1erv		41	128	1.10E-23	0.54	0.98		THIOREDOXIN; CHAIN: NULL;	OXIDOREDUCTASE DIMER, THIOREDOXIN, X-RAY CRYSTALLOGRAPHY, OXIDOREDUCTASE
709	1fb6	A	27	130	9.00E-25	0.81	1		THIOREDOXIN M; CHAIN: A; B;	ELECTRON TRANSPORT ELECTRON TRANSPORT
709	1mek		20	134	1.10E-31			82.03	PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
709	lme k		21	133	1.10E-31	0.43	0.98		PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	CENTER, ISOMERASE, 2 ENDOPLASMIC RETICULUM ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE CENTER, ISOMERASE, 2 ENDOPLASMIC RETICULUM ELECTRON TRANSPORT ALPHA/BETA OPEN-TWISTED PROTEIN, THIOL-DISULFIDE
709	lqu w	A	30	130	3.60E-24	0.62	1		THIOREDOXIN; CHAIN: A;	
709	lirp	B	26	128	1.60E-24			60.72	DNA POLYMERASE; CHAIN: A; THIOREDOXIN; CHAIN: B; DNA; CHAIN: P, T;	T7 DNA POLYMERASE, DNA REPLICATION, NUCLEOTIDYL 2 TRANSFERASE, SEQUENCING, THIOREDOXIN, PROCESSIVITY FACTOR, 3 COMPLEX (HYDROLASE/ELECTRON TRANSPORT/DNA)
709	lirp	B	27	130	1.60E-24	0.39	1		DNA POLYMERASE; CHAIN: A; THIOREDOXIN; CHAIN: B; DNA; CHAIN: P, T;	T7 DNA POLYMERASE, DNA REPLICATION, NUCLEOTIDYL 2 TRANSFERASE, SEQUENCING, THIOREDOXIN, PROCESSIVITY FACTOR, 3 COMPLEX (HYDROLASE/ELECTRON TRANSPORT/DNA)
709	lthx		24	131	9.10E-22			55.88	THIOREDOXIN; 1THX 5 CHAIN: NULL; 1THX 6	ELECTRON TRANSPORT THIOREDOXIN 2; 1THX 7 OXIDO-REDUCTASE 1THX 16
709	lthx		32	125	9.10E-22	0.75	1		THIOREDOXIN; 1THX 5 CHAIN: NULL; 1THX 6	ELECTRON TRANSPORT THIOREDOXIN 2; 1THX 7 OXIDO-REDUCTASE 1THX 16
709	ltof		25	129	9.00E-23	0.33	0.66		THIOREDOXIN H; CHAIN: NULL;	ELECTRON TRANSPORT HTRX, HCHI, CHI; OXIDOREDUCTASE, ELECTRON TRANSPORT
709	2trx A	A	24	131	5.40E-25			62.2	ELECTRON TRANSPORT THIOREDOXIN 2TRXA 2 2TRXA 3	
709	2trx A	A	25	130	5.40E-25	0.39	1		ELECTRON TRANSPORT THIOREDOXIN 2TRXA 2 2TRXA 3	
715	lasu		130	283	1.80E-25	-0.13	0.39		AVIAN SARCOMA VIRUS INTEGRASE; 1ASU 7 CHAIN:	DNA INTEGRATION

SEQ NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
715	1b9d	A	142	297	5.40E-26	0.21	0.29		NULL; 1ASU 8	TRANSFERASE DNA INTEGRATION
715	1b9f	A	142	297	5.40E-31	0.07	0.21		INTEGRASE; CHAIN: A; INTEGRASE; CHAIN: A;	TRANSFERASE DNA INTEGRATION, TRANSFERASE
715	1b3	C	142	297	5.40E-33	0	0.19		INTEGRASE; CHAIN: A, B, C;	DNA INTEGRATION DNA INTEGRATION, AIDS, POLYPROTEIN, HYDROLASE, 2 ENDONUCLEASE, POLYNUCLEOTIDYL TRANSFERASE, DNA BINDING 3 (VIRAL)
715	1c0m	A	131	337	1.30E-29	-0.06	0.1		INTEGRASE; CHAIN: A, B, C, D;	TRANSFERASE INTEGRASE, ROUS SARCOMA VIRUS, HIV, X-RAY CRYSTALLOGRAPHY, 2 PROTEIN STRUCTURE, TRANSFERASE
715	1c1a	B	139	337	3.60E-26	-0.25	0.13		RSV INTEGRASE; CHAIN: A, B;	VIRUS/VIRAL PROTEIN INTEGRASE, ROUS SARCOMA VIRUS, HIV, X-RAY CRYSTALLOGRAPHY, 2 VIRUS/VIRAL PROTEIN
715	1cxq	A	135	274	3.60E-21	0.08	0.68		AVIAN SARCOMA VIRUS INTEGRASE; CHAIN: A;	TRANSFERASE MIXED BETA-SHEET SURROUNDED BY ALPHA-HELICES
715	1exq	A	142	297	9.00E-26	0.17	0.17		POLYPROTEIN; CHAIN: A, B;	VIRUS/VIRAL PROTEIN HIV-1 INTEGRASE, POLYNUCLEOTIDYL TRANSFERASE, DNA-BINDING 2 PROTEIN, DD35E
715	1qs4	A	142	297	9.00E-28	0.41	0.39		HIV-1 INTEGRASE; CHAIN: A, B, C;	HYDROLASE DNA INTEGRATION, INTEGRASE, HIV, HYDROLASE, ASPARTYL 2 PROTEASE, ENDONUCLEASE
719	1a5e		112	228	1.30E-24	0.41	0.99		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
719	1a5e		94	197	6.50E-24	0.68	1		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
719	1awc	B	112	239	1.10E-34	0.12	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
719	1awc	B	73	230	5.40E-39			72.74	GA BINDING PROTEIN	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	REGULATION/DNA) GABPALPHA; GABPBETA1: COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
719	lawc	B	78	228	5.40E-39	0.32	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1: COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
719	lbd8		21	160	1.10E-25	-0.08	0.51		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
719	lbd8		73	233	7.80E-35			68.17	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
719	lbd8		78	218	7.80E-35	0.77	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
719	lbd8		78	231	1.10E-34	0.13	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
719	lbi7	B	112	228	1.40E-25	0.33	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
719	lbi9	B	21	160	9.00E-24	0.21	0.36		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
719	1blx	B	44	201	1.30E-35			70.26	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
719	1blx	B	78	218	1.30E-35	0.62	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
719	1blx	B	78	231	3.60E-34	0.39	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
719	1bu9	A	18	165	1.10E-25	-0.07	0.12		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
719	1bu9	A	70	239	1.10E-36			67.41	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
719	1bu9	A	78	233	1.10E-36	0.17	1		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
719	1d9s	A	101	218	2.60E-29	0.33	1		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
719	1d9s	A	112	234	1.10E-25	0.48	0.99		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
719	1d9s	A	78	197	1.20E-28	0.73	1		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
719	lih	A	1	131	1.40E-21	-0.2	0.06		CHAIN: A; CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
719	lih	A	18	164	5.40E-25	0.31	0.93		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
719	lih	A	75	232	5.40E-36			63.76	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
719	lih	A	78	232	5.40E-36	0.24	1		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
719	lik	D	107	238	3.60E-26	-0.33	0.33		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
719	lik	D	13	177	3.60E-33	-0.04	0.9		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
719	lik	D	21	216	7.20E-39			69.17	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
719	lik	D	39	228	7.20E-39	-0.05	0.69		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
719	lik	D	5	144	1.30E-27	-0.21	0.76		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
719	1myo		110	225	2.60E-28	0.14	1		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT
719	1myo		75	192	6.50E-33			64.15	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLTATION, NMR, ANK-REPEAT
719	1nfi	E	106	238	9.00E-26	0.19	0.94		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
719	1nfi	E	12	177	9.00E-33	-0.07	0.92		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
719	1nfi	E	39	228	1.10E-38	0.07	0.78		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
719	1nfi	E	7	202	1.10E-38			65.66	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
719	1lys	B	74	239	1.60E-20			64.29	P53; CHAIN: A, 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
721	1awc	B	161	312	7.80E-42	0.79	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	1awc	B	2	147	2.60E-42	0.83	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
721	lawc	B	2	147	3.60E-34	0.71	1		CHAIN: B; DNA; CHAIN: D, E;	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	226	378	5.20E-43	1.14	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	23	180	1.30E-44	0.72	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	231	378	3.60E-39	0.9	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	259	412	5.20E-45	1.23	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
721	lawc	B	264	411	5.40E-41	0.93	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	297	442	1.80E-36	0.93	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	33	180	1.30E-38	0.69	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	330	475	1.80E-36	0.67	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	363	487	7.20E-32	0.22	0.62		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA, DNA-BINDING, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
721	lawc	B	61	213	6.50E-47	0.59	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	66	213	1.40E-39	0.79	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	99	246	5.40E-38	0.87	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	1bd8		128	281	2.60E-38	0.79	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	1bd8		161	348	2.60E-38	0.12	0.42		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
721	1bd8		2	149	1.20E-40	0.43	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
721	1bd8		227	381	9.10E-41	0.73	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
721	1bd8		24	182	1.30E-41	0.53	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
721	lawc	B	61	213	6.50E-47	0.59	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	66	213	1.40E-39	0.79	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lawc	B	99	246	5.40E-38	0.87	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lbd8		128	281	2.60E-38	0.79	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
721	lbd8		161	348	2.60E-38	0.12	0.42		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
721	lbd8		2	149	1.20E-40	0.43	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
721	lbd8		227	381	9.10E-41	0.73	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
721	lbd8		24	182	1.30E-41	0.53	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
721	1bd8		263	414	1.20E-38	0.89	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	ANKYRIN MOTIF TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
721	1bd8		297	442	1.40E-30	0.74	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
721	1bd8		62	215	7.80E-44	0.67	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
721	1blx	B	132	285	1.30E-39	0.83	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
721	1blx	B	163	350	5.20E-38	0.13	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
721	1blx	B	2	153	1.00E-41	0.81	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
721	1blx	B	22	185	6.50E-43	0.61	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
721	1blx	B	230	385	1.30E-43	0.78	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
721	1blx	B	263	416	5.20E-41	1.13	1		CYCLIN-DEPENDENT	COMPLEX (INHIBITOR)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
721	1blx	B	64	252	6.50E-43	0.39	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
721	1bu9	A	33	185	7.20E-38	0.61	1		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
721	1bu9	A	330	480	1.80E-32	0.37	0.35		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
721	1bu9	A	91	258	7.20E-38			90.26	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
721	1d9s	A	14	153	6.50E-36	0.6	1		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
721	1d9s	A	250	384	1.30E-37	0.66	1		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
721	1d9s	A	283	416	1.30E-40	0.58	1		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
721	1d9s	A	52	185	2.60E-38	0.65	1		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
721	1d9s	A	84	216	2.60E-38	0.61	1		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
721	1ihb	A	297	446	1.80E-32	0.7	1		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
721	1ihb	A	33	184	3.60E-37	0.55	1		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
721	1ihb	A	330	479	1.30E-31	0.5	0.92		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
721	1ihb	A	96	250	3.60E-37			88.22	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
721	1ikn	D	127	333	2.60E-57			82.11	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I; KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
721	1ikn	D	161	386	2.60E-55	-0.02	0.93		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I; KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
721	1ikn	D	2	188	5.20E-52	0.48	0.99		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I; KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
721	1ikn	D	226	411	5.40E-43	0.56	1		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I; KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
721	1ikn	D	226	416	7.80E-52	0.55	1		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I; KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
721	1ikn	D	292	475	7.20E-39	0.4	0.39		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65; P50D;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SqFold score	Compound	PDB annotation
									CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I- KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
721	likn	D	325	486	7.20E-34	0.09	0.05		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I- KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
721	likn	D	61	233	5.40E-38	0.2	1		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I- KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
721	likn	D	61	256	2.60E-57	0.22	1		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I- KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
721	Infi	E	124	322	2.60E-52			85.42	NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
721	Infi	E	124	350	2.60E-52	0.08	1		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
721	Infi	E	2	153	7.80E-42	0.69	1		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
721	Infi	E	21	216	7.80E-53	0.49	1		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
721	Infi	E	224	411	7.20E-43	0.82	1		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
721	Infi	E	226	420	6.50E-52	0.8	1		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
721	Infi	E	292	475	1.60E-38	0.65	1		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B; D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
721	1nfi	E	323	486	1.80E-33	0.52	0.96		B, D; I-KAPPA-B-ALPHA; CHAIN: E, F; NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
723	1awc	B	107	280	1.60E-31	0.32	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
723	1awc	B	175	343	1.60E-23	0.4	0.64		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
723	1awc	B	265	408	3.60E-30	0.02	-0.17		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
723	1awc	B	31	198	5.40E-36			64.41	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
723	1awc	B	6	157	5.40E-36	0.35	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
									BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
723	lawc	B	72	212	2.60E-27	0.71	1		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
723	1bd8		38	201	3.60E-29			56.93	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
723	1bd8		43	182	7.20E-27	0.43	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
723	1bd8		9	160	3.60E-29	0.21	1		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
723	1blx	B	43	202	2.60E-26	0.44	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
723	1blx	B	9	148	5.40E-29	0.44	1		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
723	1bu9	A	107	291	3.60E-29	0.24	0.3		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
723	1bu9	A	6	162	5.40E-34	0.25	0.96		CYCLIN-DEPENDENT	HORMONE/GROWTH FACTOR P18-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									KINASE 6 INHIBITOR; CHAIN: A;	INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
723	1bu9	A	73	234	1.80E-26	0.32	0.88		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
723	1iib	A	107	284	1.80E-28	0.07	0.35		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
723	1iib	A	6	161	1.80E-33	0.15	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
723	likn	D	2	174	1.80E-43	0.13	1		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
723	likn	D	2	208	1.80E-43			61.01	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
723	likn	D	35	229	3.60E-36	0.37	0.95		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
723	likn	D	68	280	1.10E-28	-0.02	0.43		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
723	lnfi	E	136	288	5.40E-30	0.06	0.65		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
723	lnfi	E	2	174	9.00E-44	0.31	1		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: C;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
723	1nfi	E	34	229	5.40E-36	0.49	1		B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
723	1nfi	E	36	246	9.00E-44			59.74	NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
725	1a4y	A	1	369	1.30E-13	-0.4	0.07		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
725	1a4y	A	219	577	9.00E-17	-0.3	0.16		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
725	1a4y	A	267	597	2.60E-22	-0.33	0.55		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
725	1a4y	A	82	558	3.90E-36			93.46	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
725	1a4y	A	83	376	9.10E-39	0.15	1		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
725	1a9n	A	134	306	5.20E-27	-0.02	0.57		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	A	203	351	1.30E-25	0.06	0.75		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	A	430	576	3.90E-19	0.12	0.77		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	A	454	576	6.50E-20	-0.33	0.45		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	A	89	228	3.90E-29	0.22	0.99		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	C	134	319	1.20E-27	-0.06	0.84		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	C	203	351	2.60E-25	0.24	0.88		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	C	430	576	3.90E-19	-0.04	0.69		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	C	454	576	6.50E-20	0	0.45		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	C	82	213	9.10E-26	0.05	0.55		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1a9n	C	89	236	6.50E-29	0.27	0.96		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
725	1d0b	A	1	158	1.60E-26	-0.09	0.68		INTERNALIN B; CHAIN: A; INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
725	1d0b	A	104	319	1.30E-24	0.02	1		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
725	1d0b	A	216	364	5.40E-29	0.12	1		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
725	1d0b	A	242	406	9.00E-28	0.04	0.4		INTERNALIN B; CHAIN: A;	ADHESION CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
725	1d0b	A	32	166	5.40E-24	0.18	0.92		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
725	1d0b	A	415	596	1.10E-21	0.09	0.34		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
725	1dce	A	216	301	3.60E-13	0.12	1		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
725	1dce	A	246	346	5.40E-13	-0.23	0.95		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
725	1dce	A	268	369	9.00E-13	0.18	0.96		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
725	1dce	A	428	533	1.80E-13	0.08	0.22		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
725	1dce	A	475	601	7.20E-09	0.07	0.07		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
725	1ds9	A	60	170	1.30E-13	0.3	0.95		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
725	1ds9	A	17	140	3.60E-13	-0.34	0.21		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
725	1ds9	A	210	324	1.10E-14	-0.36	0.94		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
725	1ds9	A	232	346	7.20E-13	-0.73	0.12		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
725	1ds9	A	70	164	1.30E-13	-0.47	0.52		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
725	1ds9	A	82	213	3.90E-26	-0.79	0.75		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
725	1fqv	A	1	172	3.60E-07	0.02	0.04		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
725	1fqv	A	264	575	1.30E-09	-0.35	0.09		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
725	1fqv	A	84	253	1.00E-16	-0.06	0.06		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
725	1fs2	A	244	453	3.60E-11	-0.09	0.11		SKP2; CHAIN: A, C, SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
725	1fs2	A	401	577	7.80E-19	-0.12	0.27		SKP2; CHAIN: A, C, SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
725	1fs2	A	89	338	6.50E-40	-0.14	0.31		SKP2; CHAIN: A, C, SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
725	1yrg	A	211	431	1.30E-09	-0.22	0.04		GTPASE-ACTIVATING PROTEIN RNAI_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP, GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIREDIAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
725	2bnh		110	498	1.10E-19	-0.07	0.22		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
725	2bnh		239	592	5.40E-21	-0.26	0.87		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
725	2bnh		35	448	1.80E-19	-0.33	0.01		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RICH REPEATS ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE- RICH REPEATS
725	2bnh		85	558	1.10E-19			90.38	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE- RICH REPEATS
728	1awc	B	2	145	3.60E-32	0.12	-0.03		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
728	1awc	B	23	167	1.30E-35	0.19	0.29		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
728	1awc	B	27	179	1.30E-35			53.5	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
728	1awc	B	55	203	1.60E-31	0.32	0.72		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
728	1bu9	A	23	183	1.80E-29	0.33	0.01		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	3 FACTOR HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
728	1bu9	A	5	150	1.80E-29	0.28	0.09		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
728	1bu9	A	97	250	1.40E-27	0.04	-0.15		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
728	lihb	A	23	166	3.60E-29	0.25	0.41		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
728	likn	D	12	162	9.00E-37	0.15	0.24		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
728	likn	D	18	198	1.80E-32	0.27	0.23		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
728	lnfi	E	12	162	9.00E-37	0.24	0.22		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
728	lnfi	E	17	198	5.40E-32	0.16	0.36		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
728	lnfi	E	50	245	1.30E-26	0.03	0.09		NF-KAPPA-B P65; CHAIN: A; C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
728	1nfi	E	88	253	5.40E-29	0.06	0.03		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
729	1bf6	A	74	208	3.90E-07	0.37	0.69		PHOSPHOTRIESTERASE HOMOLOGY PROTEIN; CHAIN: A, B;	PHOSPHOTRIESTERASE PHOSPHOTRIESTERASE, HYPOTHETICAL PROTEIN
731	1sro		540	618	5.40E-23	0.13	1		PNPASE; CHAIN: NULL;	SI RNA-BINDING DOMAIN POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE, SI RNA-BINDING DOMAIN, POLYNUCLEOTIDE PHOSPHORYLASE 2 (PNPASE)
736	1alh	A	137	217	1.10E-26	0.08	0.82		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
736	1alh	A	361	443	7.80E-45			81.11	QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
736	1alh	A	389	469	7.80E-45	-0.04	1		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
736	1alh	A	417	498	6.50E-41	-0.33	0.9		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
736	1mey	C	136	217	1.80E-43	0.06	0.96		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
736	1mey	C	164	245	3.60E-46	0.27	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
736	1mey	C	192	273	9.00E-48	0.41	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
736	1mey	C	220	301	7.20E-49	0.19	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
736	1mey	C	276	357	9.00E-51	0.38	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
736	1mey	C	304	385	7.20E-51	0.26	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
736	1mey	C	332	413	3.60E-50	0.46	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
736	1mey	C	332	414	7.20E-51			104.61	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
736	1mey	C	360	441	9.00E-50	0.44	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
736	1mey	C	388	469	3.60E-50	0.05	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
736	1me _y	C	416	497	1.80E-50	-0.1	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
736	1tf6	A	137	282	1.40E-34	0.09	0.33		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
736	1tf6	A	193	338	1.10E-36	0.04	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
736	1tf6	A	276	444	2.60E-79			112.4	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
736	1tf6	A	333	479	3.60E-38	-0.11	0.95		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
736	1tf6	A	361	499	1.60E-35	-0.04	0.92		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
736	1ubd	C	111	217	5.40E-29	0.01	0.19		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
736	1ubd	C	162	273	1.00E-56	0.03	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
736	1ubd	C	218	329	1.30E-55	0.18	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
736	1ubd	C	246	358	1.20E-57	0.11	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
736	1ubd	C	274	385	3.90E-57	0.1	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
736	1ubd	C	304	414	3.90E-57			89.47	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
736	1ubd	C	359	469	2.60E-56	0.01	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
736	1ubd	C	368	469	1.80E-34	0	1		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
736	1ubd	C	386	497	3.90E-51	-0.18	0.96		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
736	1ubd	C	396	497	3.60E-34	-0.04	0.99		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
736	2gli	A	150	275	2.60E-58	0.2	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
736	2gli	A	164	300	1.80E-34	0.38	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
736	2gli	A	164	303	2.60E-70	0.22	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
736	2gli	A	192	359	5.20E-74	0.03	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
736	2gli	A	249	387	1.30E-73	0.58	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
736	2gli	A	250	387	5.20E-74			92.84	D; ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
736	2gli	A	305	471	2.60E-72	-0.06	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
736	2gli	A	340	468	3.60E-33	0.06	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
736	2gli	A	360	499	2.60E-68	0.03	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
736	2gli	A	368	496	3.60E-34	0.19	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
736	2gli	A	68	216	5.40E-29	-0.23	0.05		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
741	1a0q	L	20	230	7.20E-05			55.38	29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE
741	1bog	A	19	230	3.60E-05			55.09	ANTIBODY (CB 4-1); CHAIN: A, B; PEPTIDE; CHAIN: C;	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, CROSS REACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1, COMPLEX (ANTIBODY/PEPTIDE)
741	1fng	A	126	212	1.60E-17	0.19	-0.12		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
741	1ghf	L	19	230	0.0054			57.41	ANTI-ANTI-IDIOTYPE GH1002 FAB FRAGMENT; CHAIN: L, H	ANTIBODY FAB FRAGMENT ANTIBODY FAB FRAGMENT
741	1hmf		24	213	9.10E-18			69.87	T LYMPHOCYTE ADHESION	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
741	1hnf		28	199	9.10E-18	0.09	0.76		GLYCOPROTEIN CD2 (HUMAN) 1HNF 3	
741	1hng	A	25	217	2.60E-18			69.09	T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (HUMAN) 1HNF 3	
741	1hng	A	29	210	2.60E-18	0.35	0.35		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	
741	1osp	L	19	230	0.0011			55.92	FAB 184.1; CHAIN: L, H; OUTER SURFACE PROTEIN A; CHAIN: O;	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN) OSPA; COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN), OUTER SURFACE 2 PROTEIN A COMPLEXED WITH FAB184.1, BORRELIA BURGDORFERI 3 STRAIN B31
741	1tnm		131	213	3.60E-14	0.09	-0.18		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
741	2gfb	A	19	230	3.60E-05			53.4	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (CNJ206) 2GFB 3	
741	3ncm	A	22	84	1.80E-09	0	-0.18		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
747	1fqv	A	46	81	2.60E-05	-0.07	0.92		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
750	1an4	A	353	390	0.0078	-0.61	0.09		USF; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) UPSTREAM STIMULATORY FACTOR 1; USF, DNA BINDING, BASIC-HELIX-LOOP-HELIX, LEUCINE ZIPPER, 2 TRANSCRIPTION FACTOR, COMPLEX (DNA-BINDING PROTEIN/DNA)
750	1ikn	A	243	346	0.0013	0.39	0.41		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
750	1nfk	A	234	319	0.0013	-0.37	0.04		NUCLEAR FACTOR KAPPA-B; CHAIN: A, B; KB SITE, DNA (5'-D(TGAGAAATTCCTCC)-3'); CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) NF-KB P50, COMPLEX (TRANSCRIPTION FACTOR/DNA)
754	1cyg		932	1059	0.0016	-0.02	0.05		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) ICYG 3	
754	1qho	A	854	967	0.0061	0.11	0.37		ALPHA-AMYLASE; CHAIN: A;	HYDROLASE MALTOGENIC ALPHA AMYLASE, AMYLASE, GLYCOSIDE HYDROLASE, STARCH DEGRADATION
754	1ubi		1529	1617	0.0065	-0.58	0.03		CHROMOSOMAL PROTEIN UBIQUITIN IUBI 3	
756	1alh	A	229	314	3.60E-25	-0.45	0.03		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
756	1alh	A	78	162	3.60E-24	-0.33	0.03		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
756	1mey	C	134	220	1.40E-44	-0.52	0.04		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
756	1mey	C	193	284	9.00E-44	-0.6	0.06		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
756	1mey	C	379	465	3.60E-42	-0.15	0.28		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
756	1mey	C	526	612	1.10E-42	-0.19	0.12		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
756	1mey	C	555	627	3.60E-30	0.06	-0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
756	1mey	C	77	162	1.80E-42	-0.44	0.17		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
756	1mey	G	163	190	5.40E-12	0.06	0.05		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
756	1mey	G	254	284	9.00E-11	-0.3	0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
756	1mey	G	437	465	9.00E-11	0.06	-0.19		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
756	1tf3	A	349	432	1.80E-15	-0.43	0.34		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
756	1tf6	A	106	285	1.40E-34			69.84	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
756	1tf6	A	135	302	1.40E-34	-0.18	0.11		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
756	1ubd	C	139	253	1.30E-30	-0.77	0.11		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
756	1ubd	C	325	436	1.80E-27	-0.21	0.23		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
756	1ubd	C	470	578	1.80E-31	-0.72	0		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
756	1ubd	C	85	190	1.80E-30	-0.53	0.01		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
756	2adr		349	406	3.60E-15	-0.63	0.11		ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
756	2adr		498	554	1.40E-15	-0.13	0.04		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
756	2gli	A	142	286	1.10E-28	-0.53	0.07		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
									ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLL, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
757	lcun	A	537	726	7.80E-14	0.12	-0.02		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
757	lcun	A	566	749	9.10E-15	0.13	0		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
757	ldro		1096	1203	5.20E-06	0.08	0.43		BETA-SPECTRIN; IDRO 6 CHAIN: NULL; IDRO 7	CYTOSKELETON
757	lfb8	A	1093	1203	5.20E-18	0.44	0.89		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
757	lfgy	A	1097	1203	1.20E-18	0.56	0.68		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
762	lb0x	A	801	857	3.60E-12	0.04	-0.09		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN:	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION

SEQ ID NO;	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
762	1b4f	A	793	863	1.10E-14	0.1	-0.02		A;	MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
762	1sgg		797	861	7.20E-14	0.53	-0.02		EPHB2; CHAIN: A, B, C, D, E, F, G, H; EPHRII TYPE-B RECEPTOR 2; CHAIN: NULL;	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
763	1a4p	A	1	92	1.30E-20			69.57	S100A10; CHAIN: A, B;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN P11, CALPACTIN LIGHT CHAIN; S100 FAMILY, EF-HAND PROTEIN, LIGAND OF ANNEXIN II, 2 CALCIUM/PHOSPHOLIPID BINDING PROTEIN
763	1a4p	A	2	89	1.30E-20	0.67	1		S100A10; CHAIN: A, B;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN P11, CALPACTIN LIGHT CHAIN; S100 FAMILY, EF-HAND PROTEIN, LIGAND OF ANNEXIN II, 2 CALCIUM/PHOSPHOLIPID BINDING PROTEIN
763	1ak8		4	81	3.60E-21	0.11	-0.11		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERUM TRIC-DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
763	1b4c	A	1	92	7.20E-19			145.44	S-100 PROTEIN, BETA CHAIN; CHAIN: A, B;	METAL BINDING PROTEIN S100B, S100BETA; S100BETA, S100B, NMR, DIPOLAR COUPLINGS, EF-HAND, S100 2 PROTEIN, CALCIUM- BINDING PROTEIN, FOUR-HELIX BUNDLE, THREE- 3 DIMENSIONAL STRUCTURE, SOLUTION STRUCTURE
763	1cb1		3	83	7.80E-27			57.95	CALCIUM-BINDING PROTEIN CALBINDIN D9K (INTACT FORM) (NMR. 13 STRUCTURES) CBI 3	
763	1cb1		4	82	7.80E-27	0.43	0.99		CALCIUM-BINDING	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
763	1edm	A	4	81	9.00E-21	0.21	0.06		PROTEIN CALBINDIN D9K (INTACT FORM) (NMR, 13 STRUCTURES) 1CB1 3	
763	1cmf		1	81	7.20E-21	0.17	0.15		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
763	1exr	A	4	89	3.60E-23	0.06	-0.17		CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
763	1f71	A	8	81	7.20E-20	-0.17	0.18		CALMODULIN; CHAIN: A; CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
763	1mho		2	89	1.40E-16			137.02	S-100 PROTEIN; CHAIN: NULL;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
763	1top		5	92	7.20E-20	0.07	-0.07		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CALCIUM-BINDING CALCIUM-BINDING, ZINC, METAL-BINDING, ACETYLATION
766	1aj5	A	135	252	2.60E-09	-0.18	0.09		CALPAIN; CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALCIUM-BINDING PROTEIN, CALCIUM-DEPENDENT PROTEASE, APO 2 FORM, SMALL SUBUNIT
766	1dtl	A	131	252	2.60E-09	-0.29	0.28		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
766	1exr	A	129	252	1.30E-09	-0.18	0.39		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
766	1fpw	A	129	252	2.60E-08	0.05	-0.03		CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A; TROPONIN C; CHAIN: NULL;	METAL BINDING PROTEIN YEAST FREQUENIN EF-HAND, CALCIUM
766	1tcf		135	252	3.90E-10	-0.12	0.47			CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
766	1tnx		140	252	1.00E-10	-0.53	0.31		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	MUSCLE CONTRACTION CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
766	1trc	A	194	252	1.30E-08	-0.37	0.95		CALCIUM BINDING PROTEIN CALMODULIN (TR=2-CS FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	
766	5pal		177	252	1.30E-08	0.27	0.53		CALCIUM-BINDING PROTEIN PARVALBUMIN (ALPHA LINEAGE) SPAL 3	
768	1fqy	A	10	227	1.10E-73	-0.22	0.51		AQUAPORIN-1; CHAIN: A;	MEMBRANE PROTEIN AQP1 WATER CHANNEL, TWO-DIMENSIONAL CRYSTAL, ELECTRON 2 DIFFRACTION, ELECTRON MICROSCOPY
768	1fqy	A	9	227	3.90E-76	-0.13	0.88		AQUAPORIN-1; CHAIN: A;	MEMBRANE PROTEIN AQP1 WATER CHANNEL, TWO-DIMENSIONAL CRYSTAL, ELECTRON 2 DIFFRACTION, ELECTRON MICROSCOPY
769	1byn	A	541	664	1.30E-11	0.21	0.94		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
769	1dn1	B	26	252	5.20E-05	-0.13	0.01		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B; SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
769	1dqv	A	541	647	6.50E-07	0.38	0.82		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
769	1dsy	A	541	664	0.0026	0.48	0.71		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++; PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL-SERINE, PROTEIN KINASE C
769	1rsy		541	664	6.50E-12	0.3	1		CALCIUM/PHOSPHOLIPID	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
770	1bkd	S	1	311	9.10E-77			79.72	H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
770	1bkd	S	12	291	9.10E-77	0.2	1		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
770	1bkd	S	41	312	7.20E-61	0.26	1		H-RAS; CHAIN: R; SON OF SEVENLESS-1; CHAIN: S;	P21; SOS; COMPLEX (ONCOGENE PROTEIN/EXCHANGE FACTOR), SMALL GTPASE, 2 EXCHANGE FACTOR
770	1btm		438	541	1.40E-18	-0.09	0.68		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
770	1dro		439	546	7.20E-12	-0.22	0.4		BETA-SPECTRIN; IDRO 6 CHAIN: NULL; IDRO 7	CYTOSKELETON
770	1dyn	A	456	541	5.40E-06	-0.04	0.25		SIGNAL TRANSDUCTION PROTEIN DYNAMIN (PLECKSTRIN HOMOLGY DOMAIN) (DYNPH) IDYN 3	
770	1fb8	A	429	546	1.00E-07	0.3	0.9		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
770	1fb8	A	441	539	1.30E-12	0.04	0.05		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
770	1fgy	A	447	546	1.10E-16	0.35	0.36		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
770	1pls		437	542	1.10E-13	-0.02	0.24		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									PLECKSTRIN HOMOLGY DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	
772	1alh	A	131	210	6.50E-41	0.19	0.99		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
772	1alh	A	269	351	5.20E-45			78.23	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
772	1mey	C	128	209	5.40E-46	0.37	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
772	1mey	C	156	237	3.60E-47	0.29	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
772	1mey	C	184	265	1.80E-48	0.46	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
772	1mey	C	212	293	1.10E-49	0.29	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
772	1mey	C	296	377	3.60E-51	0.25	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
772	1me y	C	296	378	3.60E-51			102.88	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
772	1me y	C	324	405	3.60E-51	0.16	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
772	1me y	C	352	433	7.20E-51	0.33	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
772	1me y	C	380	461	7.20E-51	0.44	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
772	1me y	C	99	181	5.40E-43	0.04	0.42		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
772	1tf6	A	126	298	5.20E-73			115.72	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
772	1tf6	A	129	274	1.10E-36	0.22	0.76		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
772	1tf6	A	297	443	1.30E-37	0.09	0.94		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
772	1tt6	A	325	461	1.80E-36	0.15	0.96		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
772	1tt6	A	72	218	3.60E-33	-0.27	0.15		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
772	1ubd	C	120	209	3.90E-42	0.12	0.87		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
772	1ubd	C	131	237	1.80E-32	0.32	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
772	1ubd	C	133	237	6.50E-52	0.2	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
772	1ubd	C	154	266	1.30E-53	0.3	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMR score	SeqFold score	Compound	PDB annotation
772	1ubd	C	212	322	7.80E-55			89.18	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
772	1ubd	C	238	349	7.80E-55	-0.04	0.92		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
772	1ubd	C	294	405	6.50E-56	0.26	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
772	1ubd	C	304	405	1.60E-35	0.22	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
772	1ubd	C	322	434	1.30E-56	0.16	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
772	1ubd	C	350	461	5.20E-51	0.4	0.95		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
772	1ubd	C	360	461	1.80E-34	0.32	0.92		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
772	2gli	A	121	239	2.60E-54	0.21	0.88		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
772	2gli	A	128	264	3.60E-33	0.35	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
772	2gli	A	128	295	3.90E-66	0.16	0.76		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
772	2gli	A	212	351	1.00E-71			98.73	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
772	2gli	A	268	407	1.00E-71	0.4	0.93		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
772	2gli	A	304	432	7.20E-33	0.24	0.84		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
772	2gli	A	324	461	6.50E-67	0.35	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
772	2gli	A	332	460	5.40E-34	0.47	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
772	2gli	A	50	180	9.00E-28	0.07	-0.05		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
772	2gli	A	71	211	5.40E-31	-0.01	0.15		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
773	1a17		105	180	1.30E-08	0.09	0.77		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
773	1elr	A	105	180	9.10E-08	0.14	0.68		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
773	1elw	A	105	180	6.50E-10	0.12	0.74		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
773	1feh	A	105	179	6.50E-09	0.47	0.99		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
774	1a9x	A	454	860	1.80E-64	0.14	0.9		CARBAMOYL PHOSPHATE SYNTHETASE; CHAIN: A, B, C, D, E, F, G, H;	AMIDOTRANSFERASE AMIDOTRANSFERASE, THIOESTER
774	1a9x	A	529	892	1.10E-39	0.49	0.96		CARBAMOYL PHOSPHATE SYNTHETASE; CHAIN: A, B, C, D, E, F, G, H;	AMIDOTRANSFERASE AMIDOTRANSFERASE, THIOESTER
774	1b6r	A	532	858	1.80E-16	0.07	-0.11		NS-CARBOXYAMINOIMIDAZOLE RIBONUCLEOTIDE CHAIN: A;	LYASE AIRC, PURK; ATP-GRASP, CARBOXYPHOSPHATE, PURINE BIOSYNTHESIS, LYASE
774	1dv1	A	534	965	1.30E-86	0.32	0.54		BIOTIN CARBOXYLASE; CHAIN: A, B;	LIGASE ATP-GRASP, CARBOXYLASE, BIOTIN-DEPENDENT
774	1ehi	A	531	858	9.00E-37	0.07	0.45		D-ALANINE-D-LACTATE LIGASE; CHAIN: A, B;	LIGASE LMDDL2; ATP-BINDING. GRASP MOTIF FOR ATP.

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
774	1ehi	B	531	858	1.80E-36	0.22	0.63		D-ALANINE-D-LACTATE LIGASE; CHAIN: A, B;	LIGASE LMDDL2; ATP-BINDING. GRASP MOTIF FOR ATP.
774	1euc	B	656	854	7.20E-22	-0.04	0.07		SUCCINYL-COA SYNTHETASE, ALPHA CHAIN: CHAIN: A; SUCCINYL-COA SYNTHETASE, BETA CHAIN; CHAIN: B;	LIGASE SCS-ALPHA; SCS-BETA; LIGASE, GTP-SPECIFIC
774	1eyz	A	533	953	6.50E-30	0.51	0.99		PHOSPHORIBOSYLGLYCINA MIDE FORMYLTRANSFERASE 2; CHAIN: A, B;	TRANSFERASE TRANSFORMYLASE, PURINE BIOSYNTHESIS, ATP-GRASP
774	1eyz	A	534	860	1.40E-39	0.21	0.11		PHOSPHORIBOSYLGLYCINA MIDE FORMYLTRANSFERASE 2; CHAIN: A, B;	TRANSFERASE TRANSFORMYLASE, PURINE BIOSYNTHESIS, ATP-GRASP
774	1gso	A	531	898	3.60E-54	0.2	0.37		GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE; CHAIN: A;	LIGASE PURD GEN PRODUCT; GAR- SYN, GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE, ATP-GRASP, 2 PURINE DE NOVO BIOSYNTHETIC PATHWAY, SUBSTRATE CHANNELING
774	liow		530	859	1.80E-43	-0.07	0.18		D-ALA/D-ALA LIGASE; CHAIN: NULL;	LIGASE DD-LIGASE, DDLB; GLYCOGEN PHOSPHORYLASE, LIGASE, CELL WALL, PEPTIDOGLYCAN 2 SYNTHESIS, VANCOMYCIN, ADP BINDING
774	2scu	B	656	844	1.80E-27	0.04	0.07		SUCCINYL-COA LIGASE; CHAIN: A, D; SUCCINYL- COA LIGASE; CHAIN: B, E;	LIGASE SCS; SCS; CITRIC ACID CYCLE, HETEROTETRAMER, LIGASE
775	1f60	A	2	443	0	1.05	1		ELONGATION FACTOR EEF1A; CHAIN: A; ELONGATION FACTOR EEF1B; CHAIN: B;	TRANSLATION PROTEIN-PROTEIN COMPLEX
776	1aox	A	119	313	9.00E-28	0.66	1		INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
776	1aox	A	120	316	9.00E-28			84.82	INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
776	1aox	A	321	504	7.20E-28	0.74	1		INTEGRIN ALPHA 2 BETA;	INTEGRIN INTEGRIN, CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
776	1atz	A	122	293	9.00E-24	0.76	1		CHAIN: A, B; VON WILLEBRAND FACTOR; CHAIN: A, B;	ADHESION, GLYCOPROTEIN COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD
776	1atz	A	122	305	9.00E-24			94.53	VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD
776	1atz	A	324	492	1.80E-21	0.68	1		VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD
776	1auq		110	317	3.60E-32	0.42	0.69		A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
776	1auq		311	509	7.20E-29			86.49	A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
776	1auq		313	508	7.20E-29	0.78	1		A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
776	1ck4	A	122	309	1.80E-28	0.39	1		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, ADHESION
776	1ck4	A	324	500	3.60E-30	0.85	1		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, ADHESION
776	1fns	A	119	314	7.20E-31	0.27	0.75		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
776	1fns	A	319	507	3.60E-28	0.84	1		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
776	1ido		124	267	2.60E-30	0.7	1		INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
776	1ido		124	307	5.40E-27	0.62	1		INTEGRIN; CHAIN: NULL;	CYTOSKELETON CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
776	1ido		324	498	9.10E-44			96.71	INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
776	1ido		325	497	9.10E-44	0.57	1		INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
776	1ido		326	498	9.00E-26	0.54	1		INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
776	1lfa	A	123	268	3.60E-23	0.42	1		CD11A; ILFA 5 CHAIN: A, B; ILFA 6	CELL ADHESION LFA-1, ALPHA- LFA 8
776	1lfa	A	323	501	3.60E-24			90.24	CD11A; ILFA 5 CHAIN: A, B; ILFA 6	CELL ADHESION LFA-1, ALPHA- LFA 8
776	1lfa	A	326	503	3.60E-24	0.85	1		CD11A; ILFA 5 CHAIN: A, B; ILFA 6	CELL ADHESION LFA-1, ALPHA- LFA 8
776	1qc5	A	122	309	7.20E-28	0.7	1		ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
776	1qc5	A	324	499	1.60E-29	1.09	1		ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
777	1b3u	A	1	343	3.60E-33	0.02	0.17		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
777	1ee4	A	1	322	3.60E-49	0.52	1		KARYOPHERIN ALPHA;	TRANSPORT PROTEIN SERINE-RICH

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
									CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
777	1ee4	A	233	347	5.40E-10	0.03	0.17		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
777	1ial	A	1	344	1.40E-51			52.47	IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
777	1ial	A	5	343	1.40E-51	0.55	1		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
777	2bct		26	347	3.60E-39	0.26	0.98		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-CATENIN, STRUCTURAL PROTEIN
777	3bct		1	336	1.30E-29	0.3	0.94		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
777	3bct		68	347	5.40E-31	0.21	0.75		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
779	1byn	A	140	265	2.60E-39	0.41	1		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
779	1byn	A	143	264	3.60E-24	0.59	1		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
779	1dqv	A	140	376	2.60E-73	0.51	1		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
779	1dqv	A	143	387	9.00E-55	0.43	1		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
779	1rsy		136	266	2.60E-41			130.23	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
779	1rsy		140	264	2.60E-41	0.35	1		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
779	1rsy		143	264	3.60E-24	0.56	1		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
783	1alh	A	145	227	7.20E-31			70.71	QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION; OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
783	1alh	A	19	91	7.20E-22	-0.31	0.03		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION; OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
783	1alh	A	95	169	3.60E-26	-0.2	0.06		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION; OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
783	1b8t	A	88	277	7.80E-13			58.15	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
783	1ext	A	10	186	0.00026			57.16	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN; CYTOKINE, SIGNALLING PROTEIN
783	1mey	C	116	197	3.60E-50	0.32	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
783	1me y	C	144	225	3.60E-50	0.54	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
783	1me y	C	172	253	1.30E-50	0.47	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
783	1me y	C	172	254	1.30E-50			92.4	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
783	1me y	C	18	91	3.60E-39	-0.15	0.03		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
783	1me y	C	200	276	1.80E-46	0.43	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
783	1me y	C	68	141	5.40E-42	-0.51	0.03		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
783	1me y	C	94	169	1.10E-45	0.08	0.74		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
783	1tf6	A	116	275	1.30E-58			87.93	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
783	1ubd	C	116	226	3.90E-51			85.55	YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
783	1ubd	C	121	225	9.10E-47	0.1	0.87		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
783	1ubd	C	149	254	3.90E-51	-0.02	1		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
783	1ubd	C	70	197	3.60E-32	-0.12	0.46		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
783	2gli	A	116	255	3.90E-59			86.72	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
783	2gli	A	117	255	3.90E-59	0.14	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
783	2gli	A	145	267	1.30E-56	0.23	0.9		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
783	2gli	A	26	140	3.60E-26	-0.43	0.1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
784	1aww		340	403	1.00E-09	0.42	0.8		BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGX1, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA, BTK, SH3 2 DOMAIN, TRANSFERASE
784	1aze	A	348	402	2.60E-11	0.35	0.83		GRB2; CHAIN: A; SOS; CHAIN: B;	COMPLEX (ADAPTOR PROTEIN/PEPTIDE) ASH, GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; COMPLEX (ADAPTOR PROTEIN/PEPTIDE), SH3 DOMAIN, 2 GUANINE-NUCLEOTIDE RELEASING FACTOR
784	1bbz	A	350	403	3.90E-10	0.08	0.25		ABL TYROSINE KINASE; CHAIN: A, C, E, G; PEPTIDE P41; CHAIN: B, D, F, H;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE), SIGNAL TRANSDUCTION, 2 SH3 DOMAIN
784	1gbq	A	348	403	9.10E-12	0.4	0.87		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
784	1gri	A	343	400	1.80E-09	0.12	0.12		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
784	1pwt		344	403	2.60E-11	0.2	0.59		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
784	1qkw	A	349	403	1.30E-10	-0.25	0.71		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
784	1sem	A	349	400	5.40E-11	0.21	0.59		SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, ISEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR ISEM 19
785	1dn1	B	160	281	1.00E-05	-0.67	0.01		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
786	1a88	A	7	258	5.40E-45	-0.21	0.07		CHLOROPEROXIDASE L; CHAIN: A, B, C;	HALOPEROXIDASE BROMOPEROXIDASE L; HALOPEROXIDASE L; HALOPEROXIDASE, OXIDOREDUCTASE
786	1a8q		9	257	1.10E-38	-0.13	0.05		BROMOPEROXIDASE A1; CHAIN: NULL;	HALOPEROXIDASE CHLOROPEROXIDASE A1; HALOPEROXIDASE A1; HALOPEROXIDASE, OXIDOREDUCTASE
786	1a8s		7	258	7.20E-39	-0.12	0.22		CHLOROPEROXIDASE F; CHAIN: NULL;	HALOPEROXIDASE HALOPEROXIDASE F; HALOPEROXIDASE, OXIDOREDUCTASE, PROPIONATE COMPLEX
786	1brt		7	258	1.30E-39	0.14	0.28		BROMOPEROXIDASE A2; CHAIN: NULL;	HALOPEROXIDASE HALOPEROXIDASE A2; CHLOROPEROXIDASE A2; HALOPEROXIDASE, OXIDOREDUCTASE, PEROXIDASE, ALPHA/BETA 2 HYDROLASE FOLD, MUTANT M99T
786	1c4x	A	17	247	5.40E-41	-0.02	0.87		2-HYDROXY-6-OXO-6- PHENYLHEXA-2,4- Dienoate CHAIN: A;	HYDROLASE BPHD; HYDROLASE, PCB DEGRADATION
786	1cqw	A	13	257	1.80E-40	0.35	0.99		HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE 1-S BOND
786	1cwl		25	203	3.60E-11	0.09	0.03		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL- HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
786	1ehy	A	11	256	5.40E-38	0.23	0.52		SOLUBLE EPOXIDE HYDROLASE; CHAIN: A, B, C, D;	HYDROLASE HYDROLASE, ALPHA/BETA HYDROLASE FOLD, EPOXIDE DEGRADATION, 2 EPICHLOROHYDRIN
786	1ekl	A	14	258	1.10E-37	0	0.15		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
786	lek1	B	14	258	1.10E-37	-0.11	0.13		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
786	lhlg	A	5	121	1.60E-07	-0.32	0		LIPASE, GASTRIC; CHAIN: A, B;	HYDROLASE LIPASE
786	llpb	B	30	149	1.40E-06	-0.29	0		HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
786	lqge	D	25	203	3.60E-11	0.1	-0.03		TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	HYDROLASE PSEUDOMONADACEAE, CIS-PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
786	lqtr	A	8	242	1.60E-28	-0.16	0		PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE
786	4lip	D	25	161	1.60E-11	-0.09	0.01		TRIACYL-GLYCEROL- HYDROLASE; CHAIN: D, E;	LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE ANALOGUE, ENANTIOSELECTIVITY
788	lawe		462	576	1.20E-23	0.32	0.49		SOS1; CHAIN: NULL;	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION, SOS, PLECKSTRIN HOMOLOGY (PH) DOMAIN
788	lbin		728	819	9.00E-09	0.39	1		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
788	lby1	A	261	463	2.60E-41	-0.25	0.89		PIX; CHAIN: A;	TRANSPORT PROTEIN RHO-GTPASE EXCHANGE FACTOR, TRANSPORT PROTEIN
788	lby1	A	267	462	7.20E-23	-0.46	0.6		PIX; CHAIN: A;	TRANSPORT PROTEIN RHO-GTPASE EXCHANGE FACTOR, TRANSPORT PROTEIN
788	ldbh	A	261	570	1.80E-16	-0.1	0.96		HUMAN SOS 1; CHAIN: A;	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GENE REGULATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
788	1dbh	A	263	576	7.80E-58	0.12	1		HUMAN SOS 1; CHAIN: A;	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GENE REGULATION CYTOSKELETON
788	1dro		736	820	9.10E-09	0.22	0.21		BETA-SPECTRIN; IDRO 6 CHAIN: NULL; IDRO 7	
788	1dvp	A	618	674	9.00E-11	0.07	1		HEPATOCYTE GROWTH FACTOR-REGULATED TYROSINE CHAIN: A;	TRANSFERASE HRS; HRS, VHS, FYVE, ZINC FINGER, SUPERHELIX
788	1f5x	A	260	454	5.40E-24	0.14	1		RHO-GEF VAV; CHAIN: A;	SIGNALING PROTEIN I1 ALPHA-HELICES
788	1fao	A	726	816	3.60E-11	0.52	0.94		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
788	1fb8	A	484	574	1.00E-09	-0.4	0.29		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
788	1fb8	A	719	817	2.60E-18	0.63	0.99		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
788	1fb8	A	722	816	1.80E-11	0.67	0.98		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
788	1fgy	A	484	574	9.10E-08	-0.18	0.21		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
788	1fgy	A	725	821	1.10E-15	0.27	0.98		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
788	1fgy	A	729	814	7.80E-16	-0.15	0.06		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
788	1pls		728	819	1.80E-11	0.1	0.93		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	
788	1qgg	A	725	816	3.60E-05	0.64	0.76		INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWICH, SIGNAL TRANSDUCTION
788	1vfy	A	620	671	7.20E-08	0.04	0.94		PHOSPHATIDYLINOSITOL-3-PHOSPHATE BINDING FYVE CHAIN: A;	TRANSPORT PROTEIN FYVE DOMAIN, ENDOSOME MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN
788	1zbd	B	590	674	3.90E-21	0.11	0.1		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
789	1bj8		289	360	1.10E-08	-0.08	0.09		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
789	1bj8		387	477	3.60E-11	-0.09	0.13		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
789	1bj8		484	580	7.20E-11	0.14	-0.01		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
789	1bpv		288	360	3.60E-07	-0.31	0.11		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
789	1bpv		485	578	3.60E-10	-0.02	0.25		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
789	1bqu	A	195	360	7.20E-21	-0.19	0.06		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GPI30, INTERLEUKINE 6 2 RECEPTOR
789	1bqu	A	288	490	9.00E-15	0.09	-0.14		GP130; CHAIN: A, B;	BETA SUBUNIT, SIGNALING PROTEIN SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GPI30, INTERLEUKINE 6 2 RECEPTOR
789	1bqu	A	386	595	1.80E-18	0.11	-0.03		GP130; CHAIN: A, B;	BETA SUBUNIT, SIGNALING PROTEIN SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GPI30, INTERLEUKINE 6 2 RECEPTOR
789	1cfb		385	583	1.80E-26	0.03	0.24		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
789	1f6f	B	196	359	1.60E-14	-0.26	0.19		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
789	1fna		295	360	3.60E-07	-0.14	0.19		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 1FNA 3	
789	1fna		492	582	1.10E-11	0.04	0.22		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 1FNA 3	
789	1fna		504	586	1.30E-12	0.07	0.41		CELL ADHESION PROTEIN FIBRONECTIN CELL-	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
789	1fnf		192	582	5.40E-39	-0.02	0.51		ADHESION MODULE TYPE III-10 IFNA 3	
789	1fnf		194	588	5.40E-39			120.84	FIBRONECTIN; IFNF 6 CHAIN: NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
789	1fnf		288	674	9.00E-38	-0.03	0.31		FIBRONECTIN; IFNF 6 CHAIN: NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
789	1fnf		386	752	9.00E-39	0.02	-0.07		FIBRONECTIN; IFNF 6 CHAIN: NULL; IFNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18
789	1fnh	A	196	473	1.10E-19	0.11	0.07		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
789	1fnh	A	389	673	7.20E-32	0.05	0.55		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
789	1lar	A	893	1462	0	0.68	1		LAR; CHAIN: A, B;	HEPARIN AND INTEGRIN BINDING
789	1lar	B	782	1164	3.60E-81	0.34	1		LAR; CHAIN: A, B;	HYDROLASE TYROSINE PHOSPHATASE, LAR PROTEIN
789	1lar	B	924	1462	0	0.72	1		LAR; CHAIN: A, B;	HYDROLASE TYROSINE PHOSPHATASE, LAR PROTEIN
789	1mfn		292	474	5.40E-23	0.12	0.16		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2
789	1mfn		388	582	1.80E-25	-0.13	0.09		FIBRONECTIN; CHAIN: NULL;	HEPARIN-BINDING, GLYCOPROTEIN
789	1qg3	A	290	478	1.10E-17	0.18	0.1		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2
789	1qg3	A	388	588	1.40E-25	0.28	-1.41		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	HEPARIN-BINDING, GLYCOPROTEIN
789	1qg3	A	390	584	2.60E-29	0.3	0.92		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2
789	1qr4	A	292	480	9.00E-17	0.12	0.18		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, CARCINOMA, STRUCTURAL 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
										FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
789	1qr4	A	390	584	1.30E-20	0.32	0.41		TENASCIN; CHAIN: A, B;	FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
789	1rpm	A	889	1166	1.40E-89			405.81	RECEPTOR PROTEIN TYROSINE PHOSPHATASE MU; CHAIN: A, B;	RECEPTOR D1; RECEPTOR, PHOSPHATASE, SIGNAL TRANSDUCTION, ADHESION, 2 HYDROLASE
789	1rpm	A	891	1165	1.40E-89	0.85	1		RECEPTOR PROTEIN TYROSINE PHOSPHATASE MU; CHAIN: A, B;	RECEPTOR D1; RECEPTOR, PHOSPHATASE, SIGNAL TRANSDUCTION, ADHESION, 2 HYDROLASE
789	1ten		487	584	1.60E-07	0.08	0.03		CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) I TEN 3	
789	1ten		502	584	1.30E-08	0.08	0.03		CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) I TEN 3	
789	1tff		485	582	5.40E-13	0.16	0.31		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) I TTF 3	
789	2fcb	A	27	163	1.40E-10	0.03	-0.2		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
789	2fmb	A	391	480	1.60E-05	0.35	0.98		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
789	2fmb	A	490	584	1.80E-08	0.31	0.16		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
789	2shp	A	835	1164	1.40E-72	0.44	1		SHP-2; CHAIN: A, B;	ANGIOGENESIS, TYROSINE PHOSPHATASE, SHPTP-2; TYROSINE PHOSPHATASE, INSULIN SIGNALING, SH2 PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
793	1b8q	A	48	176	1.40E-11			58.72	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
793	1b8q	A	52	171	1.40E-11	0.46	0.23		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
793	1be9	A	45	163	9.00E-16			57.29	PSD-95; CHAIN: A; CRIP1; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
793	1be9	A	49	143	9.00E-16	1.06	1		PSD-95; CHAIN: A; CRIP1; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
793	1btm		299	388	3.60E-10	-0.05	0.04		BETA-SPECTRIN; IBTN 4 CHAIN: NULL; IBTN 5	SIGNAL TRANSDUCTION PROTEIN
793	1fao	A	295	385	5.40E-09	0.24	-0.13		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-CHAIN: A;	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
793	1fgy	A	199	267	0.0052	-0.65	0.05		GRP1; CHAIN: A;	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
793	1i16		27	138	3.60E-11	0.09	0.43		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMAOTTRACTANT FACTOR, PDZ DOMAIN
793	1qau	A	54	166	3.60E-10	0.5	0.99		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
793	1qau	A	56	168	2.60E-23	0.47	0.94		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
793	1qav	A	54	140	3.90E-23			77.08	ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
793	1qav	A	56	136	3.90E-23	0.87	1		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
793	1qav	A	56	139	3.60E-16	0.93	1		(RESIDUES 1-130); CHAIN: B; ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE. PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
794	1b7f	A	33	108	1.80E-16	0.84	0.81		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*Gp*Up*Up*Gp*Up*Up*U P*Up*Up*Up*Up*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
794	1cvj	A	8	109	5.40E-18	0.41	0.99		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T; HU ANTIGEN C; CHAIN: A;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX; GENE REGULATION/RNA
794	1d8z	A	34	105	1.30E-15	0.39	0.71		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
794	1ha1	1	1	103	9.00E-25	0.48	0.63		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN NUCLEAR PROTEIN
794	1ha1		34	107	1.80E-15	0.68	0.99		HNRNP A1; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN COMPLEX (RIBONUCLEOPROTEIN/RNA)
794	1um	A	33	112	2.60E-15	0.55	0.94		U1A SPLICEOSOMAL PROTEIN; 1URN 5 CHAIN: A, B, C; 1URN 6 RNA 21MER HAIRPIN (5'- (AP*AP*UP*CP*CP*AP*UP*U P* 1URN 11 CHAIN: P, Q, R 1URN 13	
794	2mss	A	35	103	1.60E-15	0.82	0.88		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
794	2sxl		33	108	1.80E-16	0.31	0.68		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA-BINDING DOMAIN, ALTERNATIVE SPLICING
794	2upl	A	1	111	5.40E-30	0.68	0.23		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
794	3sxl	A	33	105	5.40E-16	0.61	0.96		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
795	1am9	A	59	131	2.60E-13	0.23	0.04		STEROL REGULATORY ELEMENT BINDING PROTEIN 1A; CHAIN: A, B, C, D; DNA; CHAIN: E, F, G, H;	COMPLEX (TRANSCRIPTION REGULATION/DNA) SREBP-1A; STEROL REGULATORY ELEMENT BINDING PROTEIN, 2 BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, SREBP, TRANSCRIPTION 3 FACTOR, COMPLEX (TRANSCRIPTION REGULATION/DNA)
795	1am9	B	55	119	1.30E-15	0.14	0.27		STEROL REGULATORY ELEMENT BINDING PROTEIN 1A; CHAIN: A, B, C, D; DNA; CHAIN: E, F, G, H;	COMPLEX (TRANSCRIPTION REGULATION/DNA) SREBP-1A; STEROL REGULATORY ELEMENT BINDING PROTEIN, 2 BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, SREBP, TRANSCRIPTION 3 FACTOR, COMPLEX (TRANSCRIPTION REGULATION/DNA)
795	1an2	A	57	119	9.00E-15	0.35	-0.03		MAX PROTEIN; CHAIN: A, C; DNA; CHAIN: B, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) MYN PROTEIN; MAX, DNA BINDING, BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, 2 TRANSCRIPTION FACTOR, COMPLEX (DNA-BINDING PROTEIN/DNA)
795	1an4	A	55	115	1.80E-13	-0.08	0.07		USF; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) UPSTREAM

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
										STIMULATORY FACTOR 1; USE, DNA BINDING, BASIC-HELIX-LOOP-HELIX, LEUCINE ZIPPER, 2 TRANSCRIPTION FACTOR, COMPLEX (DNA-BINDING PROTEIN/DNA)
795	1hlo	A	53	119	3.60E-15	0.06	0.17		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D(*CP*AP*CP*CP*AP*CP*GP*TP*GP*GP*T)-3', CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)
795	1hlo	B	55	119	7.20E-15	-0.17	0.05		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D(*CP*AP*CP*CP*AP*CP*GP*TP*GP*GP*T)-3', CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)
795	Imdy	B	53	114	1.40E-14	0.15	-0.11		TRANSCRIPTION ACTIVATION/DNA MYOD BASIC-HELIX-LOOP-HELIX (BHLH) DOMAIN IMDY 3 (RESIDUES 102 - 166) MUTANT WITH CYS 135 REPLACED BY SER IMDY 4 (C135S) COMPLEXED WITH DNA IMDY 5 (5'-D(*TP*CP*AP*AP*CP*AP*GP*CP*TP*GP*TP*TP*GP*A)-3') IMDY 6	
800	1alh	A	327	405	1.40E-22	0.07	-0.19		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
800	1alh	A	353	433	3.60E-26	0.24	0.55		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
800	1alh	A	357	434	5.20E-32	0.31	0.42		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLICATION OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
800	Ime	C	352	433	5.40E-44	0.14	0.68		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
	y								CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	1me y	C	380	461	1.80E-46	0.49	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	1me y	C	381	461	3.90E-48	0.45	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	1me y	C	408	489	2.60E-48	0.52	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	1me y	C	408	489	5.40E-47	0.52	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	1me y	C	436	517	9.00E-48	0.48	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	1me y	C	464	545	1.80E-48	0.45	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	1me y	C	492	573	9.00E-50	0.15	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	1me y	C	520	601	1.80E-50	0.19	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
800	Imey	C	548	629	5.40E-51	0.3	1		PROTEIN; CHAIN: C, F, G; DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	Imey	C	576	657	3.60E-51	0.21	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	Imey	C	576	658	3.60E-51			107.23	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	Imey	C	604	685	5.40E-51	0.38	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	Imey	C	632	713	1.20E-51	0.54	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	Imey	C	632	713	1.40E-50	0.54	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	Imey	C	660	741	1.40E-50	0.41	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
800	Imey	C	688	765	9.00E-46	0.19	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
800	1tf3	A	292	377	3.60E-11	0	-0.2		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	CRYSTAL STRUCTURE; COMPLEX (ZINC FINGER/DNA)
800	1tf6	A	353	498	1.80E-35	0.2	0.54		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
800	1tf6	A	521	666	9.00E-38	0.31	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
800	1tf6	A	576	741	7.20E-38			111.83	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
800	1tf6	A	605	754	7.20E-38	-0.13	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
800	1ubd	C	332	433	1.30E-28	-0.16	0.43		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	355	461	5.40E-31	0.15	0.96		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	357	461	1.30E-45	0.05	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	385	489	1.30E-57	0.51	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	434	545	7.80E-55	0.1	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	490	601	1.30E-53	0.12	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	528	629	9.00E-35	0.33	0.93		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
800	1ubd	C	546	657	1.30E-58	0.11	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	548	658	5.20E-60			91.29	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	556	657	3.60E-35	0.22	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	602	713	5.20E-60	0.25	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	612	713	1.60E-34	0.13	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
800	1ubd	C	630	741	3.90E-61	0.15	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
800	2gli	A	367	463	1.30E-43	0.44	0.93		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
800	2gli	A	380	519	3.90E-71			105.23	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
800	2gli	A	381	547	2.60E-70	0.18	0.88		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
800	2gli	A	408	603	3.90E-71	0.06	0.81		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
800	2gli	A	464	631	5.20E-73	0.15	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
800	2gli	A	528	656	1.30E-34	0.16	0.9		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
800	2gli	A	576	743	5.20E-79	0.11	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
800	2gli	A	584	712	5.40E-34	0.32	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
800	2gli	A	612	743	1.10E-33	0.41	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C; D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
804	1cun	A	91	302	0.0052	-0.2	0.37		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
804	1dov	A	79	257	3.90E-59	0.41	1			TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
804	1dow	A	54	257	6.50E-70	0.37	1		ALPHA-CATENIN; CHAIN: A;	CELL ADHESION FOUR-HELIX BUNDLE
804	1eh1	A	367	441	0.0072	-0.65	0.06		ALPHA-CATENIN; CHAIN: A; BETA-CATENIN; CHAIN: B;	CELL ADHESION FOUR-HELIX BUNDLE
804	1fxk	A	5	103	1.30E-06	-0.34	0.01		RIBOSOME RECYCLING FACTOR; CHAIN: A;	RIBOSOME TRANSLATION, RIBOSOME, HINGE VARIABILITY
									PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	CHAPERONE ARCHAEAL PROTEIN
808	1a3p		3949	3984	6.50E-12	0.39	0.58		EPIDERMAL GROWTH FACTOR; CHAIN: NULL;	GROWTH FACTOR [ABUG, 20] MEGF4-48; GROWTH FACTOR, MURINE EPIDERMAL GROWTH FACTOR, DISULFIDE 2 CONNECTIVITIES, EGF-LIKE DOMAIN, REPEAT
808	1aut	L	3943	4033	6.50E-19	0.55	-0.12		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
808	1bf9		3949	3987	1.30E-11	0.96	0.99		FACTOR VII; CHAIN: NULL;	BLOOD COAGULATION BLOOD COAGULATION, EGF, HYDROLASE, SERINE PROTEASE
808	1c4r	A	3771	3928	1.30E-26	0.26	0.4		NEUREXIN-I BETA; CHAIN: A, B, C, D, E, F, G, H;	MEMBRANE PROTEIN LECTIN-LIKE, NEUROBIOLOGY, CELL-CELL ADHESION, CELL-CELL 2 RECOGNITION, ALTERNATIVE SPLICING, MEMBRANE PROTEIN
808	1d2s	A	3773	3934	2.60E-27	0.46	0.72		SEX HORMONE-BINDING GLOBULIN; CHAIN: A;	TRANSPORT PROTEIN SHBG; STEROID TRANSPORT, LAMININ G-LIKE DOMAIN, JELLYROLL, 2 ANDROGEN BINDING PROTEIN (ABP), SEX STEROID BINDING PROTEIN 3 (SBP)
808	1dva	L	3944	4033	3.90E-21	0.48	0.05		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1dva	L	4263	4344	1.30E-13	0.25	-0.18		(LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y; DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
808	1dx5	I	4232	4336	1.30E-11	0.06	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H; E-CADHERIN; CHAIN: A, B;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
808	1edh	A	1066	1234	3.60E-33	0.26	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1171	1338	1.30E-32	0.22	1202.08		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1279	1440	3.60E-21	0.45	0.9		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1352	1547	1.60E-49	0.27	0.82		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1460	1652	1.30E-32	0.1	-1.41		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1edh	A	1589	1750	3.60E-33	0.21	0.96		E-CADHERIN; CHAIN: A, B;	AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1690	1860	1.60E-28	0.19	0.99		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1800	1960	3.60E-26	0.32	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	182	354	1.60E-20	0	0		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1898	2062	3.60E-29	0.26	0.96		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1975	2163	1.10E-50	0.3	0.51		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2104	2264	1.30E-28	0.24	0.78		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2178	2371	3.60E-48	0.18	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
808	1edh	A	2306	2473	1.60E-35	0.32	1		E-CADHERIN; CHAIN: A, B;	ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2414	2577	1.80E-29	0.07	0.86		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN
808	1edh	A	2488	2683	1.80E-38	0	0.93		E-CADHERIN; CHAIN: A, B;	EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2619	2789	5.40E-32	0.1	0.96		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN
808	1edh	A	2692	2895	1.80E-57			120.62	E-CADHERIN; CHAIN: A, B;	EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2693	2898	1.80E-57	0.47	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN
808	1edh	A	2831	3003	7.20E-35	0.27	1		E-CADHERIN; CHAIN: A, B;	EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2941	3105	5.40E-29	0.31	0.94		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1edh	A	296	450	7.20E-25	0.38	0.53		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	3046	3197	5.40E-28	0.16	0.64		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	3120	3313	1.80E-32	0.57	-1.41		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	3225	3418	1.80E-48	0.45	0.98		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	3355	3523	3.60E-30	0.66	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	39	248	1.80E-51	0.12	0.3		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	406	556	1.10E-29	0.29	0.83		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	464	662	3.60E-29	0.17	0.82		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1edh	A	591	812	5.40E-22	-0.05	0.27		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	718	917	1.10E-55	0.33	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	854	1022	1.10E-32	0.31	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	959	1129	9.00E-32	0.11	0.69		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1em n		3946	4022	1.80E-16	0.71	0.99		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
808	1fsb		3949	3988	1.30E-11	1.03	0.88		P-SELECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN EGF-LIKE DOMAIN, CELL ADHESION PROTEIN, TRANSMEMBRANE, 2 GLYCOPROTEIN
808	1klo		3924	4050	1.10E-13	-0.1	0.27		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
808	1klo		3954	4075	5.40E-21	0.07	-0.03		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
808	1klo		4201	4342	3.60E-17	0.23	-0.2		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
808	1ncg		1062	1127	9.00E-06	0.12	0.29		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1ncg		1167	1232	0.00014	0.13	0.69		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1ncg		1350	1439	1.40E-14	0.01	0.29		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1ncg		1480	1546	0.00018	0.46	0.1		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	Incg		155	229	3.60E-05	0.15	0.09		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		1599	1650	9.00E-06	-0.13	0.09		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		1667	1748	3.60E-06	0.35	0.31		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		1970	2061	3.60E-17	0.22	0.1		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		2079	2161	0.00036	0.28	0.11		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		2178	2263	3.60E-12	-0.08	0.1		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		2304	2370	1.80E-06	0.41	0.74		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		2411	2458	0.00036	-0.27	0.43		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		2593	2681	1.60E-05	0.34	0.57		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		2692	2788	1.80E-19	0.44	0.7		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		2913	2988	0.00054	0.35	0.39		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		3039	3106	3.60E-06	0.45	0.51		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		3120	3191	1.80E-05	0.06	0.34		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		3225	3311	1.60E-11	0.33	0.36		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		716	811	7.20E-20	0.16	0.8		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		852	900	0.00018	-0.19	0.53		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Incg		932	1003	5.40E-05	0.38	0.64		N-CADHERIN; INCG 3	INCG 13 CELL ADHESION PROTEIN CADHERIN
808	Inc1	B	1065	1129	1.80E-06	0.06	0.78		N-CADHERIN; INC1 3	INC1 13 CELL ADHESION PROTEIN CADHERIN
808	Inc1	B	1172	1234	5.40E-05	0.06	0.96		N-CADHERIN; INC1 3	INC1 13 CELL ADHESION PROTEIN CADHERIN
808	Inc1	B	1350	1440	1.30E-13	0.43	0.22		N-CADHERIN; INC1 3	INC1 13 CELL ADHESION PROTEIN CADHERIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	Inci	B	1491	1547	0.00018	-0.08	0.65		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	1667	1750	9.00E-07	0.35	0.6		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	181	248	1.60E-05	-0.17	0.4		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	1970	2062	1.80E-16	0.08	0.23		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2116	2163	0.0013	-0.25	0.05		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2178	2264	1.30E-11	-0.11	0.1		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2307	2371	5.40E-07	0.17	0.75		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2414	2458	0.0009	-0.14	0.58		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2620	2683	1.60E-05	0	0.06		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2692	2789	3.60E-19	0.56	1.		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2942	3003	0.0036	0.42	0.92		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	3044	3105	5.40E-06	0.56	0.42		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	3146	3191	0.00036	-0.2	0.17		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	3225	3313	1.80E-10	0.67	0.49		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	3354	3418	1.80E-08	0.87	0.99		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	715	812	1.80E-19	0.15	0.96		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	862	917	5.40E-05	-0.4	0.71		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	932	1022	1.80E-05	0.36	0.63		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	A	1039	1234	3.60E-36	0.45	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	Inci	A	1147	1338	5.40E-33	0.34	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	Inci	A	1270	1440	1.80E-22	0.3	0.54		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1ncj	A	1351	1547	3.60E-53	0.29	0.99		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	1458	1652	1.80E-34	0.03	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	155	354	5.40E-24	0.05	0.21		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	1562	1750	3.60E-33	0.45	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	1667	1861	3.60E-32	-0.05	0.74		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	1782	1960	7.20E-27	0.31	0.96		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	1898	2062	3.60E-28	0.42	0.76		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	1970	2163	7.20E-55	0.11	0.33		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2079	2264	3.60E-30	0.48	0.86		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	2178	2371	5.40E-52	0.17	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2300	2473	5.40E-36	0.27	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	2407	2577	7.20E-32	-0.1	0.75		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2488	2683	1.60E-41	0.14	0.83		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	256	450	3.60E-27	0.25	0.3		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2593	2789	1.30E-32	0.29	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	2691	2897	5.40E-63			120.25	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2693	2898	5.40E-63	0.28	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	2825	3003	3.60E-38	0.31	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2913	3105	1.80E-29	0.62	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	3039	3196	1.40E-31	-0.03	0.58		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1ncj	A	3120	3313	1.80E-34	0.36	0.63		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	3225	3418	7.20E-51	0.48	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	3346	3523	3.60E-32	0.63	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	3433	3621	3.60E-13	0.52	0.39		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	39	248	1.80E-57	-0.28	0.21		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	390	556	1.80E-34	0.3	0.35		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	467	662	9.00E-30	0.37	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	571	812	1.80E-25	0.02	0.18		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	717	917	7.20E-62	0.23	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	827	1022	1.80E-34	0.34	0.88		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	932	1129	1.10E-34	0.39	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1pfx	L	4224	4312	1.40E-10	0.01	-0.19		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/VEGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
808	1qfk	L	3943	4001	1.30E-11	0.2	-0.19		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
808	1qfk	L	3951	4033	1.20E-21	0.68	0.57		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1qfk	L	4121	4202	5.40E-14	0	-0.17		INHIBITOR; CHAIN: C; COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
808	1qfk	L	4267	4344	7.20E-13	0.37	-0.17		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
808	1rfn	B	3951	4001	7.80E-14	0.03	-0.19		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
808	1suh		1041	1133	7.80E-20	0.24	0.27		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1066	1133	1.60E-07	-0.06	0.93		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1145	1238	1.30E-17	0.04	0.45		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1249	1334	1.30E-10	0.54	0.62		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1279	1342	0.0013	0.28	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1350	1444	1.80E-19	0.37	0.04		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1455	1549	1.30E-08	0.45	0.63		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		155	226	2.60E-07	0.35	0.07		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1suh		1570	1650	1.00E-12	0.41	0.31		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1589	1656	9.00E-09	-0.2	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1667	1754	1.30E-12	0.07	0.68		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1690	1754	3.60E-06	0.17	0.75		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1777	1867	1.30E-14	-0.06	0.48		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1800	1868	3.60E-05	-0.18	0.45		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		182	252	1.80E-06	-0.41	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2084	2163	2.60E-15	0.42	0.09		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2178	2268	1.30E-15	-0.37	0.4		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2280	2375	3.90E-20	0.44	0.77		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2306	2375	3.60E-09	0.35	0.94		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2395	2475	3.90E-05	0.03	0.58		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2414	2477	3.60E-05	-0.04	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2488	2581	1.80E-12	-0.37	0.15		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI- BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1suh		2489	2581	1.30E-13	0.16	0.98		EPITHELIAL CADHERIN; CHAIN: NULL;	ADHESION CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2591	2681	2.60E-10	0.02	0.12		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2692	2793	3.60E-23	0.42	0.99		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2806	2902	2.60E-21	0.43	0.87		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2831	2902	3.60E-09	0.01	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2914	3007	1.20E-14	0.37	0.93		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2941	3007	1.80E-06	-0.07	0.86		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3026	3109	2.60E-21	0.36	0.89		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3046	3109	3.60E-06	0.4	0.72		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3120	3185	0.0013	0.1	0.28		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3120	3213	3.90E-12	0.43	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3225	3317	1.10E-14	0.6	0.82		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3330	3422	3.90E-21	0.58	0.98		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3355	3422	1.30E-09	0.66	0.93	8	EPITHELIAL CADHERIN;	CELL ADHESION UVOMORULIN;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
									CHAIN: NULL;	CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3435	3524	6.50E-11	0.56	0.65		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		363	454	0.0001	0.08	0.24		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		406	454	1.60E-05	-0.6	0.19		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		467	560	1.30E-15	-0.03	0.19		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		590	658	3.90E-05	0.39	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		716	816	1.40E-23	-0.21	0.95		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		826	921	1.00E-17	0.4	0.72		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		854	921	5.40E-07	0.17	0.45		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		930	1026	5.20E-13	0.37	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1tpg		3949	4026	1.30E-18	0.21	0.59		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
808	1xka	L	4267	4348	5.40E-12	0.15	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
808	9wga	A	4166	4337	3.60E-10	0.05	-0.2		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
808	1aut	L	3857	3947	6.50E-19	0.55	-0.12		ACTIVATED PROTEIN C;	COMPLEX (BLOOD

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COAGULATION/INHIBITOR AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
808	1dan	L	3831	3897	1.40E-12	0.09	0.07		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE- ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
808	1dan	L	3900	3976	3.60E-14	0.1	0.07		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE- ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
808	1dva	L	3831	3897	1.40E-12	-0.08	0.15		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
808	1dva	L	3858	3947	3.90E-21	0.48	0.05		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
808	1dva	L	3900	3976	3.60E-14	0.12	-0.07		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
808	1dva	L	4078	4168	3.60E-12	0.05	-0.15		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H; I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L; M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
808	1dva	L	4170	4259	1.30E-13	0.25	-0.19		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H; I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L; M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
808	1edh	A	1026	1234	1.10E-33	0.35	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1171	1338	9.00E-30	0.16	0.96		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1279	1440	1.60E-20	0.23	0.93		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1352	1547	3.60E-54	0.3	0.89		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1455	1652	7.20E-32	0.03	0.65		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1589	1750	3.60E-33	0.19	-1.41		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1edh	A	1690	1860	3.60E-28	-0.18	0.25		E-CADHERIN; CHAIN: A, B;	AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1780	1960	1.80E-27	0.21	0.99		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	182	354	5.40E-20	0.17	0.07		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1898	2062	1.80E-30	0.3	0.94		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	1975	2163	1.80E-50	0.13	0.34		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2104	2264	9.00E-29	0.19	0.92		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2178	2371	1.80E-38	0.08	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2306	2473	1.80E-32	0.37	-1.41		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
808	1edh	A	2414	2577	3.60E-29	0.07	0.86		E-CADHERIN; CHAIN: A, B;	ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2488	2683	1.60E-39	0.14	0.75		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2619	2789	7.20E-31	0.33	0.99		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2692	2895	5.40E-58			120.62	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2693	2898	5.40E-58	0.52	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2831	3003	1.80E-33	0.46	- 1202.08		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	2941	3105	1.80E-28	0.31	0.94		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	296	450	5.40E-24	0.15	0.41		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1edh	A	3045	3191	1.80E-27	0.28	0.6		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	3147	3313	1.80E-28	0.15	0.59		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	3225	3418	1.40E-35	0.53	0.98		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	3355	3523	1.80E-16	0.47	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	39	248	3.60E-53	0.12	0.3		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	401	556	5.40E-30	0.31	0.89		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	465	662	3.60E-27	0.5	0.77		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	718	917	1.10E-57	0.33	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
808	1edh	A	854	1022	1.80E-33	0.14	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1edh	A	959	1129	1.80E-30	0.24	0.52		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
808	1em n		3860	3931	3.60E-16	0.06	0.48		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
808	1em n		4126	4217	9.00E-14	0.02	-0.18		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
808	1fak L	L	3900	3976	3.60E-14	0.12	-0.01		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
808	1fak L	L	4170	4259	1.30E-13	0.2	-0.19		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
808	1klo		4074	4228	1.80E-17	0.07	-0.2		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN BLOOD CLOTTING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1klo		4134	4262	1.80E-18	0.07	-0.2		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
808	1neg		1064	1127	1.60E-05	0.12	0.63		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		1169	1232	5.40E-05	0.15	0.87		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		1350	1439	3.60E-17	0.34	0.3		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		1455	1546	5.40E-05	0	0.72		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		155	229	3.60E-05	0.15	0.09		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		1599	1651	9.00E-06	-0.45	0.04		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		1667	1748	3.60E-06	0.35	0.31		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		1975	2061	1.80E-15	-0.06	0.1		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		2079	2161	0.00036	0.31	0.29		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		2180	2262	9.00E-07	0.11	0.01		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		2304	2369	1.80E-06	0.43	0.64		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		2411	2458	0.0045	-0.23	0.22		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		2592	2681	0.00014	0.41	0.25		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		2692	2788	3.60E-20	0.44	0.7		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		3039	3106	9.00E-07	0.45	0.51		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		3120	3191	0.00018	0.06	0.34		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		3225	3312	1.10E-12	0.28	0.45		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		716	811	1.10E-21	0.16	0.8		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		852	900	0.00036	-0.19	0.53		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
808	1neg		932	1021	1.60E-05	0.55	0.46		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
808	Inci	B	1065	1129	3.60E-06	0.06	0.78		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	1178	1234	1.80E-05	-0.16	0.9		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	1350	1440	3.60E-16	0.53	0.06		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	1481	1547	5.40E-05	0.21	0.16		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	1667	1750	1.40E-06	0.26	0.64		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	181	248	5.40E-05	-0.17	0.4		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	1912	1960	0.0045	-0.5	0.27		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	1975	2062	1.80E-14	0.24	0.07		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2180	2264	3.60E-06	-0.4	0.3		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2307	2371	5.40E-07	0.39	0.6		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2412	2458	0.0079	-0.03	0.49		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2692	2789	1.80E-19	0.56	1		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2832	2898	1.80E-06	-0.01	0		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	2951	3003	0.0045	-0.24	0.78		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	3041	3105	1.10E-06	0.52	0.66		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	3146	3191	0.0013	-0.2	0.17		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	3225	3313	1.40E-10	0.31	0.17		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	716	812	5.40E-20	0.01	0.88		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	853	917	7.20E-05	0.26	0.84		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	B	932	1022	7.20E-06	0.4	0.59		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
808	Inci	A	1039	1234	1.10E-35	0.39	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1ncj	A	1144	1338	1.40E-31	0.53	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	1251	1440	1.80E-23	0.1	0.16		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	1351	1547	1.60E-58	0.28	0.99		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	1455	1652	3.60E-35	0.02	0.88		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	1562	1750	1.10E-33	0.46	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	1667	1861	7.20E-33	0.2	0.84		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	173	354	3.60E-22	0.08	0.23		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	1793	1960	9.00E-27	0.31	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	1898	2062	3.60E-31	0.25	0.9		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	1975	2163	1.60E-56	0.02	0.45		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2079	2264	9.00E-31	0.23	0.89		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	2180	2371	3.60E-40	0.25	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2300	2473	3.60E-35	0.32	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	2407	2577	9.00E-31	-0.03	0.8		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2488	2683	3.60E-40	0.06	0.6		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	256	450	1.30E-26	0.28	0.51		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2592	2789	1.40E-31	0.23	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	2691	2897	3.60E-63			120.25	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
808	1ncj	A	2693	2898	3.60E-63	0.28	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
808	1ncj	A	2825	3003	9.00E-36	0.28	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1ncj	A	2915	3105	9.00E-30	0.35	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	3039	3196	1.30E-30	0.16	0.8		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	3141	3313	1.30E-30	0.35	0.82		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	3225	3418	1.80E-39	0.66	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	3349	3523	1.80E-17	0.6	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	3473	3621	5.40E-10	0.35	-0.03		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	39	248	1.10E-59	-0.28	0.21		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	390	556	1.80E-35	0.08	0.36		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	467	662	7.20E-28	0.36	0.96		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	573	812	1.80E-25	-0.13	0.01		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	717	917	1.10E-63	0.39	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	827	1022	1.80E-34	0.35	0.88		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1ncj	A	932	1129	3.60E-34	0.48	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
808	1qfk	L	3865	3947	1.20E-21	0.68	0.57		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
808	1qfk	L	3904	3976	3.60E-13	0.01	-0.08		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
808	1qfk	L	4082	4168	7.20E-11	0.08	-0.15		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	
808	1suh		1026	1133	7.20E-08	0.33	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1041	1133	7.80E-20	0.24	0.27		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1145	1238	1.30E-17	0.04	0.45		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1171	1238	7.20E-08	-0.03	0.4		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1249	1334	1.30E-10	0.54	0.62		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1350	1444	1.80E-21	0.3	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1455	1549	1.30E-08	0.45	0.63		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1455	1551	5.40E-07	0.14	0.11		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		155	226	2.60E-07	0.35	0.07		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1570	1650	1.00E-12	0.41	0.31		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1589	1656	1.40E-08	0.2	0.09		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1667	1754	1.30E-12	0.07	0.68		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1690	1754	3.60E-06	0.06	0.66		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1suh		1777	1867	1.30E-14	-0.06	0.48		EPITHELIAL CADHERIN; CHAIN: NULL;	ADHESION CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1780	1868	3.60E-05	-0.24	0.39		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		182	252	5.40E-07	-0.41	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1898	1964	1.60E-05	-0.1	0.18		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		1975	2066	7.20E-18	0.17	1202.08		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2084	2163	2.60E-15	0.42	0.09		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2104	2167	3.60E-07	0.05	0.12		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2178	2268	1.30E-14	-0.23	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2178	2268	3.60E-10	-0.36	0.46		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2280	2375	3.90E-20	0.44	0.77		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2306	2375	1.10E-08	0.4	0.94		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2395	2475	3.90E-05	0.03	0.58		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2414	2477	0.00011	-0.37	0.06		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2488	2581	3.60E-12	-0.2	0.03		EPITHELIAL CADHERIN;	CELL ADHESION UVOMORULIN;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: NULL;	CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2489	2581	1.30E-13	0.16	0.98		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2591	2681	2.60E-10	0.02	0.12		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2692	2793	1.40E-23	0.51	0.99		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2806	2902	2.60E-21	0.43	0.87		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2831	2902	1.40E-08	-0.01	0.53		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2914	3007	1.20E-14	0.37	0.93		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		2941	3007	1.80E-05	-0.07	0.86		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3026	3109	2.60E-21	0.36	0.89		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3045	3109	3.60E-06	0.33	0.55		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3120	3213	3.90E-12	0.43	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3225	3317	1.30E-13	0.6	0.82		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3330	3422	3.90E-21	0.58	0.98		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		3355	3422	5.40E-05	0.6	0.94		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
808	1suh		3435	3524	6.50E-11	0.56	0.65		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		363	454	0.0001	0.08	0.24		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		401	454	9.00E-06	-0.21	0.3		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		467	560	1.30E-15	-0.03	0.19		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		590	658	3.90E-05	0.39	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		716	816	7.20E-25	-0.21	0.95		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		826	921	1.00E-17	0.4	0.72		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		854	921	1.30E-07	0.27	0.47		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		930	1026	5.20E-13	0.37	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1suh		959	1026	9.00E-07	0.2	0.18		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
808	1tpg		3863	3940	1.30E-18	0.21	0.59		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
808	1xka	L	3904	3994	7.20E-11	-0.26	0.1		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
808	9wga	A	4069	4234	5.40E-12	0.02	-0.2		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1a3p		3949	3984	6.50E-12	0.39	0.58		EPIDERMAL GROWTH FACTOR; CHAIN: NULL;	GROWTH FACTOR [ABU6, 20] MEGF4-48; GROWTH FACTOR, MURINE EPIDERMAL GROWTH FACTOR, DISULFIDE 2 CONNECTIVITIES, EGF-LIKE DOMAIN, REPEAT
809	1aut	L	3943	4033	6.50E-19	0.55	-0.12		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA, HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
809	1bf9		3949	3987	1.30E-11	0.96	0.99		FACTOR VII; CHAIN: NULL;	BLOOD COAGULATION BLOOD COAGULATION, EGF, HYDROLASE, SERINE PROTEASE
809	1c4r	A	3771	3928	1.30E-26	0.26	0.4		NEUREXIN-J BETA; CHAIN: A, B, C, D, E, F, G, H;	MEMBRANE PROTEIN LECTIN-LIKE, NEUROBIOLOGY, CELL-CELL ADHESION, CELL-CELL 2 RECOGNITION, ALTERNATIVE SPLICING, MEMBRANE PROTEIN
809	1d2s	A	3773	3934	2.60E-27	0.46	0.72		SEX HORMONE-BINDING GLOBULIN; CHAIN: A;	TRANSPORT PROTEIN SHBG; STEROID TRANSPORT, LAMININ G-LIKE DOMAIN, JELLYROLL, 2 ANDROGEN BINDING PROTEIN (ABP), SEX STEROID BINDING PROTEIN 3 (SBP)
809	1dva	L	3944	4033	3.90E-21	0.48	0.05		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
809	1dva	L	4263	4344	1.30E-13	0.25	-0.18		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1dx5	I	4232	4336	1.30E-11	0.06	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
809	1edh	A	1066	1234	3.60E-33	0.26	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1171	1338	1.30E-32	0.22	-1202.08		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1279	1440	3.60E-21	0.45	0.9		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1352	1547	1.60E-49	0.27	0.82		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1460	1652	1.30E-32	0.1	-1.41		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1589	1750	3.60E-33	0.21	0.96		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1690	1860	1.60E-28	0.19	0.99		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1edh	A	1800	1960	3.60E-26	0.32	1		E-CADHERIN; CHAIN: A, B;	ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	182	354	1.60E-20	0	0		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1898	2062	3.60E-29	0.26	0.96		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1975	2163	1.10E-50	0.3	0.51		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2104	2264	1.30E-28	0.24	0.78		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2178	2371	3.60E-48	0.18	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2306	2473	1.60E-35	0.32	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2414	2577	1.80E-29	0.07	0.86		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1edh	A	2488	2683	1.80E-38	0	0.93		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2619	2789	5.40E-32	0.1	0.96		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2692	2895	1.80E-57			120.62	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2693	2898	1.80E-57	0.47	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2831	3003	7.20E-35	0.27	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2941	3105	5.40E-29	0.31	0.94		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	296	450	7.20E-25	0.38	0.53		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	3046	3197	5.40E-28	0.16	0.64		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1edh	A	3120	3313	1.80E-32	0.57	-1.41		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	3225	3418	1.80E-48	0.45	0.98		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	3355	3523	3.60E-30	0.66	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	39	248	1.80E-51	0.12	0.3		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	406	556	1.10E-29	0.29	0.83		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	464	662	3.60E-29	0.17	0.82		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	591	812	5.40E-22	-0.05	0.27		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	718	917	1.10E-55	0.33	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	854	1022	1.10E-32	0.31	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1edh	A	959	1129	9.00E-32	0.11	0.69		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1em		3946	4022	1.80E-16	0.71	0.99		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
809	1fsb		3949	3988	1.30E-11	1.03	0.88		P-SELECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN EGF-LIKE DOMAIN, CELL ADHESION PROTEIN, TRANSMEMBRANE, 2 GLYCOPROTEIN
809	1klo		3924	4050	1.10E-13	-0.1	0.27		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
809	1klo		3954	4075	5.40E-21	0.07	-0.03		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
809	1klo		4201	4342	3.60E-17	0.23	-0.2		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
809	1ncg		1062	1127	9.00E-06	0.12	0.29		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		1167	1232	0.00014	0.13	0.69		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		1350	1439	1.40E-14	0.01	0.29		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		1480	1546	0.00018	0.46	0.1		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		155	229	3.60E-05	0.15	0.09		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		1599	1650	9.00E-06	-0.13	0.09		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		1667	1748	3.60E-06	0.35	0.31		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		1970	2061	3.60E-17	0.22	0.1		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		2079	2161	0.00036	0.28	0.11		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	Incg		2178	2263	3.60E-12	-0.08	0.1		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2304	2370	1.80E-06	0.41	0.74		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2411	2458	0.00036	-0.27	0.43		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2593	2681	1.60E-05	0.34	0.57		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2692	2788	1.80E-19	0.44	0.7		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2913	2988	0.00054	0.35	0.39		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		3039	3106	3.60E-06	0.45	0.51		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		3120	3191	1.80E-05	0.06	0.34		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		3225	3311	1.60E-11	0.33	0.36		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		716	811	7.20E-20	0.16	0.8		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		852	900	0.00018	-0.19	0.53		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		932	1003	5.40E-05	0.38	0.64		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Inci	B	1065	1129	1.80E-06	0.06	0.78		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	1172	1234	5.40E-05	0.06	0.96		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	1350	1440	1.30E-13	0.43	0.22		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	1491	1547	0.00018	-0.08	0.65		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	1667	1750	9.00E-07	0.35	0.6		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	181	248	1.60E-05	-0.17	0.4		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	1970	2062	1.80E-16	0.08	0.23		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2116	2163	0.0013	-0.25	0.05		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2178	2264	1.30E-11	-0.11	0.1		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
809	Inci	B	2307	2371	5.40E-07	0.17	0.75		N-CADHERIN; INCI 3	INCI 13
809	Inci	B	2414	2458	0.0009	-0.14	0.58		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2620	2683	1.60E-05	0	0.06		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2692	2789	3.60E-19	0.56	1		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2942	3003	0.0036	0.42	0.92		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	3044	3105	5.40E-06	0.56	0.42		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	3146	3191	0.00036	-0.2	0.17		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	3225	3313	1.80E-10	0.67	0.49		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	3354	3418	1.80E-08	0.87	0.99		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	715	812	1.80E-19	0.15	0.96		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	862	917	5.40E-05	-0.4	0.71		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	932	1022	1.80E-05	0.36	0.63		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inej	A	1039	1234	3.60E-36	0.45	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inej	A	1147	1338	5.40E-33	0.34	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inej	A	1270	1440	1.80E-22	0.3	0.54		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inej	A	1351	1547	3.60E-53	0.29	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inej	A	1438	1652	1.80E-34	0.03	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inej	A	155	354	5.40E-24	0.05	0.21		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inej	A	1562	1750	3.60E-33	0.45	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inej	A	1667	1861	3.60E-32	-0.05	0.74		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1ncj	A	1782	1960	7.20E-27	0.31	0.96		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	1898	2062	3.60E-28	0.42	0.76		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	1970	2163	7.20E-55	0.11	0.33		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	2079	2264	3.60E-30	0.48	0.86		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	2178	2371	5.40E-52	0.17	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	2300	2473	5.40E-36	0.27	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	2407	2577	7.20E-32	-0.1	0.75		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	2488	2683	1.60E-41	0.14	0.83		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	256	450	3.60E-27	0.25	0.3		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	2593	2789	1.30E-32	0.29	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	2691	2897	5.40E-63			120.25	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	2693	2898	5.40E-63	0.28	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	2825	3003	3.60E-38	0.31	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	2913	3105	1.80E-29	0.62	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	3039	3196	1.40E-31	-0.03	0.58		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	3120	3313	1.80E-34	0.36	0.63		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	3225	3418	7.20E-51	0.48	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	3346	3523	3.60E-32	0.63	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	3433	3621	3.60E-13	0.52	0.39		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	39	248	1.80E-57	-0.28	0.21		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	390	556	1.80E-34	0.3	0.35		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1ncj	A	467	662	9.00E-30	0.37	0.99		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	571	812	1.80E-25	0.02	0.18		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	717	917	7.20E-62	0.23	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1ncj	A	827	1022	1.80E-34	0.34	0.88		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
809	1ncj	A	932	1129	1.10E-34	0.39	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
809	1pfx	L	4224	4312	1.40E-10	0.01	-0.19		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	ADHESION PROTEIN
809	1qfk	L	3943	4001	1.30E-11	0.2	-0.19		COAGULATION FACTOR VIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/VEGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
809	1qfk	L	3951	4033	1.20E-21	0.68	0.57		COAGULATION FACTOR VIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
809	1qfk	L	4121	4202	5.40E-14	0	-0.17		COAGULATION FACTOR VIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
809	1qfk	L	4267	4344	7.20E-13	0.37	-0.17		COAGULATION FACTOR VIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIA (HEAVY CHAIN);	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1rfn	B	3951	4001	7.80E-14	0.03	-0.19		CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C; COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
809	1suh		1041	1133	7.80E-20	0.24	0.27		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1066	1133	1.60E-07	-0.06	0.93		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1145	1238	1.30E-17	0.04	0.45		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1249	1334	1.30E-10	0.54	0.62		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1279	1342	0.0013	0.28	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1350	1444	1.80E-19	0.37	0.04		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1455	1549	1.30E-08	0.45	0.63		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		155	226	2.60E-07	0.35	0.07		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1570	1650	1.00E-12	0.41	0.31		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1589	1656	9.00E-09	-0.2	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1667	1754	1.30E-12	0.07	0.68		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1690	1754	3.60E-06	0.17	0.75		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1suh		1777	1867	1.30E-14	-0.06	0.48		EPITHELIAL CADHERIN; CHAIN: NULL;	ADHESION CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1800	1868	3.60E-05	-0.18	0.45		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		182	252	1.80E-06	-0.41	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2084	2163	2.60E-15	0.42	0.09		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2178	2268	1.30E-15	-0.37	0.4		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2280	2375	3.90E-20	0.44	0.77		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2306	2375	3.60E-09	0.35	0.94		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2395	2475	3.90E-05	0.03	0.58		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2414	2477	3.60E-05	-0.04	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2488	2581	1.80E-12	-0.37	0.15		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2489	2581	1.30E-13	0.16	0.98		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2591	2681	2.60E-10	0.02	0.12		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2692	2793	3.60E-23	0.42	0.99		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2806	2902	2.60E-21	0.43	0.87		EPITHELIAL CADHERIN;	CELL ADHESION UVOMORULIN;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: NULL;	CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2831	2902	3.60E-09	0.01	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2914	3007	1.20E-14	0.37	0.93		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2941	3007	1.80E-06	-0.07	0.86		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3026	3109	2.60E-21	0.36	0.89		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3046	3109	3.60E-06	0.4	0.72		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3120	3185	0.0013	0.1	0.28		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3120	3213	3.90E-12	0.43	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3225	3317	1.10E-14	0.6	0.82		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3330	3422	3.90E-21	0.58	0.98		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3355	3422	1.30E-09	0.66	0.93		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3435	3524	6.50E-11	0.56	0.65		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		363	454	0.0001	0.08	0.24		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		406	454	1.60E-05	-0.6	0.19		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1suh		467	560	1.30E-15	-0.03	0.19		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		590	658	3.90E-05	0.39	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		716	816	1.40E-23	-0.21	0.95		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		826	921	1.00E-17	0.4	0.72		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		854	921	5.40E-07	0.17	0.45		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		930	1026	5.20E-13	0.37	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1tpg		3949	4026	1.30E-18	0.21	0.59		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
809	1xka	L	4267	4348	5.40E-12	0.15	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
809	9wga	A	4166	4337	3.60E-10	0.05	-0.2		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
809	1aut	L	3857	3947	6.50E-19	0.55	-0.12		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO- MAI; CHAIN: P;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
809	1dan	L	3831	3897	1.40E-12	0.09	0.07		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE- ARG.	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1dan	L	3900	3976	3.60E-14	0.1	0.07		CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C; BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C; DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
809	1dva	L	3831	3897	1.40E-12	-0.08	0.15		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
809	1dva	L	3858	3947	3.90E-21	0.48	0.05		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
809	1dva	L	3900	3976	3.60E-14	0.12	-0.07		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
809	1dva	L	4078	4168	3.60E-12	0.05	-0.15		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
809	1dva	L	4170	4259	1.30E-13	0.25	-0.19		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
809	1edh	A	1026	1234	1.10E-33	0.35	1		M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y; E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1171	1338	9.00E-30	0.16	0.96		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1279	1440	1.60E-20	0.23	0.93		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1352	1547	3.60E-54	0.3	0.89		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1455	1652	7.20E-32	0.03	0.65		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1589	1750	3.60E-33	0.19	-1.41		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1690	1860	3.60E-28	-0.18	0.25		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1780	1960	1.80E-27	0.21	0.99		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1edh	A	182	354	5.40E-20	0.17	0.07		E-CADHERIN; CHAIN: A, B;	ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1898	2062	1.80E-30	0.3	0.94		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	1975	2163	1.80E-50	0.13	0.34		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2104	2264	9.00E-29	0.19	0.92		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2178	2371	1.80E-38	0.08	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2306	2473	1.80E-32	0.37	-1.41		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2414	2577	3.60E-29	0.07	0.86		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	2488	2683	1.60E-39	0.14	0.75		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1edh	A	2619	2789	7.20E-31	0.33	0.99		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM
809	1edh	A	2692	2895	5.40E-58			120.62	E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM
809	1edh	A	2693	2898	5.40E-58	0.52	1		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM
809	1edh	A	2831	3003	1.80E-33	0.46	1202.08		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM
809	1edh	A	2941	3105	1.80E-28	0.31	0.94		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM
809	1edh	A	296	450	5.40E-24	0.15	0.41		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM
809	1edh	A	3045	3191	1.80E-27	0.28	0.6		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM
809	1edh	A	3147	3313	1.80E-28	0.15	0.59		E-CADHERIN; CHAIN: A, B;	BINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1edh	A	3225	3418	1.40E-35	0.53	0.98		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	3355	3523	1.80E-16	0.47	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	39	248	3.60E-53	0.12	0.3		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	401	556	5.40E-30	0.31	0.89		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	465	662	3.60E-27	0.5	0.77		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	718	917	1.10E-37	0.33	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	854	1022	1.80E-33	0.14	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1edh	A	959	1129	1.80E-30	0.24	0.52		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
809	1em		3860	3931	3.60E-16	0.06	0.48		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	n									MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
809	1em n		4126	4217	9.00E-14	0.02	-0.18		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
809	1fak L	L	3900	3976	3.60E-14	0.12	-0.01		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTting COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTting
809	1fak L	L	4170	4259	1.30E-13	0.2	-0.19		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTting COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTting
809	1klo		4074	4228	1.80E-17	0.07	-0.2		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
809	1klo		4134	4262	1.80E-18	0.07	-0.2		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
809	1ncg		1064	1127	1.60E-05	0.12	0.63		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		1169	1232	5.40E-05	0.15	0.87		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		1350	1439	3.60E-17	0.34	0.3		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		1455	1546	5.40E-05	0	0.72		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	1ncg		155	229	3.60E-05	0.15	0.09		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	Incg		1599	1651	9.00E-06	-0.45	0.04		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		1667	1748	3.60E-06	0.35	0.31		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		1975	2061	1.80E-15	-0.06	0.1		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2079	2161	0.00036	0.31	0.29		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2180	2262	9.00E-07	0.11	0.01		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2304	2369	1.80E-06	0.43	0.64		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2411	2458	0.0045	-0.23	0.22		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2592	2681	0.00014	0.41	0.25		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		2692	2788	3.60E-20	0.44	0.7		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		3039	3106	9.00E-07	0.45	0.51		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		3120	3191	0.00018	0.06	0.34		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		3225	3312	1.10E-12	0.28	0.45		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		716	811	1.10E-21	0.16	0.8		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		852	900	0.00036	-0.19	0.53		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Incg		932	1021	1.60E-05	0.55	0.46		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
809	Inci B	B	1065	1129	3.60E-06	0.06	0.78		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci B	B	1178	1234	1.80E-05	-0.16	0.9		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci B	B	1350	1440	3.60E-16	0.53	0.06		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci B	B	1481	1547	5.40E-05	0.21	0.16		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci B	B	1667	1750	1.40E-06	0.26	0.64		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci B	B	181	248	5.40E-05	-0.17	0.4		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	Inci	B	1912	1960	0.0045	-0.5	0.27		N-CADHERIN; INCI 3	INCI 13
809	Inci	B	1975	2062	1.80E-14	0.24	0.07		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2180	2264	3.60E-06	-0.4	0.3		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2307	2371	5.40E-07	0.39	0.6		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2412	2458	0.0079	-0.03	0.49		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2692	2789	1.80E-19	0.56	1		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2832	2898	1.80E-06	-0.01	0		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	2951	3003	0.0045	-0.24	0.78		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	3041	3105	1.10E-06	0.52	0.66		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	3146	3191	0.0013	-0.2	0.17		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	3225	3313	1.40E-10	0.31	0.17		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	716	812	5.40E-20	0.01	0.88		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	853	917	7.20E-05	0.26	0.84		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	B	932	1022	7.20E-06	0.4	0.59		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
809	Inci	A	1039	1234	1.10E-35	0.39	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inci	A	1144	1338	1.40E-31	0.53	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inci	A	1251	1440	1.80E-23	0.1	0.16		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inci	A	1351	1547	1.60E-58	0.28	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inci	A	1455	1652	3.60E-35	0.02	0.88		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	Inci	A	1562	1750	1.10E-33	0.46	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1ncj	A	1667	1861	7.20E-33	0.2	0.84		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	173	354	3.60E-22	0.08	0.23		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	1793	1960	9.00E-27	0.31	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	1898	2062	3.60E-31	0.25	0.9		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	1975	2163	1.60E-56	0.02	0.45		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2079	2264	9.00E-31	0.23	0.89		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2180	2371	3.60E-40	0.25	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2300	2473	3.60E-35	0.32	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2407	2577	9.00E-31	-0.03	0.8		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2488	2683	3.60E-40	0.06	0.6		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	256	450	1.30E-26	0.28	0.51		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2592	2789	1.40E-31	0.23	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2691	2897	3.60E-63			120.25	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2693	2898	3.60E-63	0.28	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2825	3003	9.00E-36	0.28	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	2915	3105	9.00E-30	0.35	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	3039	3196	1.30E-30	0.16	0.8		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	3141	3313	1.30E-30	0.35	0.82		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	3225	3418	1.80E-39	0.66	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	3349	3523	1.80E-17	0.6	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
809	1ncj	A	3473	3621	5.40E-10	0.35	-0.03		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1ncj	A	39	248	1.10E-59	-0.28	0.21		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN CELL ADHESION PROTEIN CELL
809	1ncj	A	390	556	1.80E-35	0.08	0.36		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN CELL ADHESION PROTEIN CELL
809	1ncj	A	467	662	7.20E-28	0.36	0.96		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN CELL ADHESION PROTEIN CELL
809	1ncj	A	573	812	1.80E-25	-0.13	0.01		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN CELL ADHESION PROTEIN CELL
809	1ncj	A	717	917	1.10E-63	0.39	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN CELL ADHESION PROTEIN CELL
809	1ncj	A	827	1022	1.80E-34	0.35	0.88		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN CELL ADHESION PROTEIN CELL
809	1ncj	A	932	1129	3.60E-34	0.48	1		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN CELL ADHESION PROTEIN CELL
809	1qfk	L	3865	3947	1.20E-21	0.68	0.57		COAGULATION FACTOR VIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIA (HEAVY CHAIN); CHAIN: H; TRIPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
809	1qfk	L	3904	3976	3.60E-13	0.01	-0.08		COAGULATION FACTOR VIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIA (HEAVY CHAIN); CHAIN: H; TRIPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
809	1qfk	L	4082	4168	7.20E-11	0.08	-0.15		COAGULATION FACTOR VIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIA (HEAVY CHAIN); CHAIN: H; TRIPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
809	1suh		1026	1133	7.20E-08	0.33	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1041	1133	7.80E-20	0.24	0.27		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1145	1238	1.30E-17	0.04	0.45		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1suh		1171	1238	7.20E-08	-0.03	0.4		EPITHELIAL CADHERIN; CHAIN: NULL;	ADHESION CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1249	1334	1.30E-10	0.54	0.62		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1350	1444	1.80E-21	0.3	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1455	1549	1.30E-08	0.45	0.63		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1455	1551	5.40E-07	0.14	0.11		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		155	226	2.60E-07	0.35	0.07		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1570	1650	1.00E-12	0.41	0.31		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1589	1656	1.40E-08	0.2	0.09		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1667	1754	1.30E-12	0.07	0.68		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1690	1754	3.60E-06	0.06	0.66		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1777	1867	1.30E-14	-0.06	0.48		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1780	1868	3.60E-05	-0.24	0.39		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		182	252	5.40E-07	-0.41	0.13		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		1898	1964	1.60E-05	-0.1	0.18		EPITHELIAL CADHERIN;	CELL ADHESION UVOMORULIN;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1suh		1975	2066	7.20E-18	0.17	1202.08		CHAIN: NULL;	CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2084	2163	2.60E-15	0.42	0.09		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2104	2167	3.60E-07	0.05	0.12		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2178	2268	1.30E-14	-0.23	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2178	2268	3.60E-10	-0.36	0.46		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2280	2375	3.90E-20	0.44	0.77		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2306	2375	1.10E-08	0.4	0.94		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2395	2475	3.90E-05	0.03	0.58		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2414	2477	0.00011	-0.37	0.06		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2488	2581	3.60E-12	-0.2	0.03		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2489	2581	1.30E-13	0.16	0.98		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2591	2681	2.60E-10	0.02	0.12		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2692	2793	1.40E-23	0.51	0.99		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1suh		2806	2902	2.60E-21	0.43	0.87		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2831	2902	1.40E-08	-0.01	0.53		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2914	3007	1.20E-14	0.37	0.93		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		2941	3007	1.80E-05	-0.07	0.86		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3026	3109	2.60E-21	0.36	0.89		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3045	3109	3.60E-06	0.33	0.55		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3120	3213	3.90E-12	0.43	0.25		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3225	3317	1.30E-13	0.6	0.82		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3330	3422	3.90E-21	0.58	0.98		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3355	3422	5.40E-05	0.6	0.94		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		3435	3524	6.50E-11	0.56	0.65		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		363	454	0.0001	0.08	0.24		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		401	454	9.00E-06	-0.21	0.3		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		467	560	1.30E-15	-0.03	0.19		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
809	1suh		590	658	3.90E-05	0.39	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	ADHESION CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		716	816	7.20E-25	-0.21	0.95		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		826	921	1.00E-17	0.4	0.72		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		854	921	1.30E-07	0.27	0.47		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		930	1026	5.20E-13	0.37	0.57		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1suh		959	1026	9.00E-07	0.2	0.18		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
809	1tpg		3863	3940	1.30E-18	0.21	0.59		T-PLASMINOGEN ACTIVATOR FI-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
809	1xka	L	3904	3994	7.20E-11	-0.26	0.1		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
809	9wga	A	4069	4234	5.40E-12	0.02	-0.2		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
811	1edh	A	190	370	3.60E-24	-0.26	0.25		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
811	1edh	A	23	145	1.80E-17	0.35	0.16		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
811	1edh	A	296	474	1.80E-30	0.21	0.82		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
811	1edh	A	410	584	7.20E-26	0.21	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
811	1edh	A	50	237	1.80E-51	0.61	1		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
811	1edh	A	50	254	1.80E-51			124.11	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
811	1ncg		188	238	0.00018	0.07	0.03		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
811	1ncg		408	473	1.80E-06	0.34	0.63		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
811	1ncg		48	143	1.60E-19	0.16	1		N-CADHERIN; INCG 3	CELL ADHESION PROTEIN CADHERIN INCG 13
811	1nci	B	189	238	0.00036	-0.15	0.12		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
811	1nci	B	409	474	3.60E-07	0.44	0.62		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
811	1nci	B	48	145	5.40E-19	0.35	1		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN CADHERIN INCI 13
811	1ncj	A	160	370	1.10E-26	0.21	0.98		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
811	1ncj	A	24	145	3.60E-20	0.31	0.59		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
811	1ncj	A	271	474	1.80E-31	0.31	0.58		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
811	1ncj	A	402	566	7.20E-28	0.24	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
811	1ncj	A	49	238	1.80E-55	0.29	1		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
811	1ncj	A	49	253	1.80E-55			125.8	N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
811	1suh		162	258	1.20E-16	0.22	0.18		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
811	1suh		190	237	0.0041	-0.08	0.23		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
811	1suh		268	371	5.20E-12	0.36	0.01		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
811	1suh		383	478	1.30E-17	0.3	0.46		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
811	1suh		410	478	1.60E-08	-0.15	0.89		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
811	1suh		48	149	9.00E-23	0.65	1		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
811	1suh		49	149	2.60E-29	0.58	1		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
811	1suh		490	584	1.00E-08	0.23	0.1		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
813	1alh	A	62	142	2.60E-35	0.61	1		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, DNA-BINDING PROTEIN
813	1alh	A	69	142	3.60E-27	0.68	0.92		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, DNA-BINDING PROTEIN
813	1mey	C	117	198	7.20E-49	0.34	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION. PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
813	1mey	C	145	226	5.40E-50	0.51	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
813	1mey	C	173	254	1.80E-49	0.32	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
813	1mey	C	201	282	1.30E-49	0.34	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
813	1mey	C	201	283	1.30E-49			111.37	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
813	1mey	C	229	310	1.30E-49	0.27	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
813	1mey	C	68	142	9.00E-43	0.63	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
813	1mey	C	89	170	1.10E-48	0.39	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
813	1paa		286	312	9.00E-05	0.13	0.34		TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADR1 (RESIDUES 130 - 159) 1PAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									DOMAIN) MUTANT WITH IPAA 4 PRO 131 REPLACED BY ALA; PRO 133 REPLACED BY ALA; CYS 140 IPAA 5 REPLACED BY ALA (P131A,P133A,C140A) (NMR, 10 STRUCTURES) IPAA 6 SPIF2; CHAIN: NULL;	
813	1sp2		286	312	5.40E-07	0.27	0.35			ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER TRANSCRIPTION ACTIVATION, SP1
813	1tf6	A	118	270	1.80E-38	0.17	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
813	1tf6	A	145	310	2.60E-61			111.05	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
813	1tf6	A	174	312	9.00E-36	0.36	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
813	1tf6	A	90	235	7.20E-37	0.38	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
813	1ubd	C	144	254	2.60E-49	0.26	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
813	1ubd	C	153	254	3.60E-35	0.25	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
813	1ubd	C	172	283	1.30E-50			105.14	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
813	1ubd	C	178	283	7.80E-50	0.03	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
813	1ubd	C	199	310	1.30E-50	0.37	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
813	1ubd	C	66	170	2.60E-43	0.49	0.94		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
813	1ubd	C	69	170	1.80E-33	0.34	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
813	1ubd	C	97	198	1.80E-34	0.62	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
813	2adr		62	116	2.60E-23	0.74	1		ADR1; CHAIN: NULL;	(TRANSCRIPTION REGULATION/DNA) TRANSCRIPTION REGULATION
813	2gli	A	145	284	3.90E-62			107.07	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
813	2gli	A	145	312	3.90E-62	0.23	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
813	2gli	A	181	309	5.40E-34	0.39	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
813	2gli	A	62	172	3.90E-43	0.41	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
813	2gli	A	73	169	1.30E-30	0.42	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
813	2gli	A	89	256	9.10E-60	0.4	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
813	2gli	A	97	225	1.80E-33	0.45	0.94		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
814	1g6q	1	2	288	9.00E-58	-0.02	0.34		HNRNP ARGinine N-	TRANSFERASE SAM-BINDING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
817	1b3u	A	235	520	1.20E-07	0.32	0.98		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
817	1crz	A	821	1078	0.0036	0.16	0.03		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
817	1etj	A	796	1099	3.60E-60	0.12	1		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
817	1etj	A	831	1147	3.60E-68	0.28	1		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
817	1got	B	758	1096	3.60E-60	0.18	1		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
817	1got	B	823	1144	3.60E-73	0.63	1		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
817	1qbk	B	198	653	5.20E-05	-0.04	0.07		KARYOPHERIN BETA2; CHAIN: B; RAN; CHAIN: C;	NUCLEAR TRANSPORT PROTEIN COMPLEX HEAT REPEATS, NUCLEAR TRANSPORT PROTEIN COMPLEX
817	3bet		345	653	2.60E-15	-0.02	0.23		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
818	1dkg	A	51	222	5.20E-41			78.03	NUCLEOTIDE EXCHANGE FACTOR GRPE; CHAIN: A, B; MOLECULAR CHAPERONE	COMPLEX (HSP24/HSP70) HSP70, GRPE, MOLECULAR CHAPERONE, NUCLEOTIDE EXCHANGE 2 FACTOR,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
818	1dkg	A	53	221	1.80E-20	-0.15	0.83		DNAK; CHAIN: D;	COILED-COIL, COMPLEX (HSP24/HSP70)
818	1dkg	A	61	220	5.20E-41	-0.29	0.42		NUCLEOTIDE EXCHANGE FACTOR GRPE; CHAIN: A, B; MOLECULAR CHAPERONE DNAK; CHAIN: D;	COMPLEX (HSP24/HSP70) HSP70, GRPE, MOLECULAR CHAPERONE, NUCLEOTIDE EXCHANGE 2 FACTOR, COILED-COIL, COMPLEX (HSP24/HSP70)
820	1an2	A	135	203	3.60E-14	-0.73	0.03		MAX PROTEIN; CHAIN: A, C; DNA; CHAIN: B, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) MYN PROTEIN; MAX, DNA BINDING, BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, 2 TRANSCRIPTION FACTOR, COMPLEX (DNA-BINDING PROTEIN/DNA)
820	1an2	A	140	219	2.60E-13	-0.8	0.09		MAX PROTEIN; CHAIN: A, C; DNA; CHAIN: B, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) MYN PROTEIN; MAX, DNA BINDING, BASIC-HELIX-LOOP-HELIX-LEUCINE ZIPPER, 2 TRANSCRIPTION FACTOR, COMPLEX (DNA-BINDING PROTEIN/DNA)
820	1hlo	A	131	203	1.60E-14	-0.58	0		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D(*CP*AP*CP*CP*AP*CP*GP*TP*GP*GP*T)-3', CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)
820	1hlo	B	132	203	1.80E-14	-0.27	0.28		TRANSCRIPTION FACTOR MAX; CHAIN: A, B; DNA (5'-D(*CP*AP*CP*CP*AP*CP*GP*TP*GP*GP*T)-3', CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR MAX/DNA) TRANSCRIPTIONAL REGULATION, DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR MAX/DNA)
824	1b3u	A	44	373	6.50E-08	0.55	1		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
824	1ibr	B	131	235	0.0026	0.25	0.82		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
824	1ibr	B	201	303	6.50E-06	0.06	0.47		CHAIN: B, D; RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D; BETA-CATENIN; CHAIN: NULL;	TRANSPORT RECEPTOR SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
824	3bct		154	404	6.50E-14	0.41	0.99			
826	1b8g	A	70	294	5.40E-14	0.41	0.22		1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE; CHAIN: A, B;	LYASE ACC SYNTHASE, S-ADENOSYL-L-METHIONINE ETHYLENE BIOSYNTHESIS
826	1b9h	A	97	317	3.60E-37	0.12	-0.13		3-AMINO-5-HYDROXYBENZOIC ACID SYNTHASE; CHAIN: A;	RIFAMYCIN BIOSYNTHESIS (RIFD GENE) AHBA SYNTHASE; RIFAMYCIN BIOSYNTHESIS (RIFD GENE)
826	1bj4	A	1	312	5.40E-50	0.25	0		SERINE HYDROXYMETHYL TRANSFERASE; CHAIN: A;	TRANSFERASE TRANSFERASE, METABOLIC ROLE, PYRIDOXAL 5'-PHOSPHATE
826	1bjw	A	3	309	1.80E-52	0.29	1202.08		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL ENZYME
826	1bs0	A	1	317	7.20E-06			52.33	8-AMINO-7-OXONANOATE SYNTHASE; CHAIN: A;	TRANSFERASE AONS, 8-AMINO-7-KETOPELARGONATE SYNTHASE; PLP-DEPENDENT ACYL-COA SYNTHASE, BIOTIN BIOSYNTHESIS, 8-2 AMINO-7-OXONANOATE SYNTHASE, 8-AMINO-7-KETOPELARGONATE 3 SYNTHASE, TRANSFERASE
826	1c0n	A	10	311	9.00E-57	0.51	1		CSDB PROTEIN; CHAIN: A;	LYASE ALPHA/BETA FOLD
826	1cjo	A	1	312	3.60E-51	0.04	-1.41		SERINE HYDROXYMETHYL TRANSFERASE; CHAIN: A, B;	TRANSFERASE SHMT; HYDROXYMETHYL TRANSFERASE, 1 CARBON METABOLISM
826	1cll	A	93	314	3.60E-16	0.1	-0.19		CYSTATHIONINE BETA-LYASE; CHAIN: A, B;	METHIONINE BIOSYNTHESIS BETA CYSTATHIONASE; PLP-DEPENDENT ENZYMES, METHIONINE BIOSYNTHESIS, C-S BETA 2 LYASE
826	1cs1	A	22	313	5.40E-34	0.2	-0.03		CYSTATHIONINE GAMMA-SYNTHASE; CHAIN: A, B, C, D;	LYASE CGS; LYASE, LLP-DEPENDENT ENZYMES, METHIONINE BIOSYNTHESIS
826	1d2f	A	135	259	1.80E-09	-0.06	0.51		MALY PROTEIN; CHAIN: A, B;	TRANSFERASE AMINOTRANSFERASE FOLD, LARGE PLP-BINDING DOMAIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
826	1dfo	A	8	314	9.00E-54	-0.07	0.17		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D;	SMALL C-2 TERMINAL DOMAIN, OPEN ALPHA-BETA STRUCTURE. TRANSFERASE SHMT, SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD
826	1eg5	A	32	317	3.60E-58	0.62	1		AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE PLP-DEPENDENT ENZYMES, IRON-SULFUR-CLUSTER SYNTHESIS, C-S 2 BETA LYASE
826	1ejj	A	1	312	5.40E-50	0.09	-1.41		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT; SERINE-GLYCINE CONVERSION, PYRIDOXAL 5'-PHOSPHATE, 2
826	1qgn	A	50	311	7.20E-21	0.19	-0.06		CYSTATHIONINE GAMMA-SYNTHASE; CHAIN: A, B, C, D, E, F, G, H;	TETRAHYDROFOLATE, ASYMMETRIC DIMER
826	1tpl	A	101	311	3.60E-09	0.21	-0.03		LYASE(CARBON-CARBON) TYROSINE PHENOL-LYASE (E.C.4.1.99.2) ITPL 3	LYASE METHIONINE BIOSYNTHESIS, PYRIDOXAL 5'-PHOSPHATE, GAMMA-2 FAMILY, LYASE
826	2tpl	A	101	311	1.30E-08	0.02	-0.06		TYROSINE PHENOL-LYASE; CHAIN: A, B;	LYASE LYASE, PLP-DEPENDENT ENZYME, PYRIDOXAL PHOSPHATE
830	1c4z	A	1213	1566	1.10E-45			217.98	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
830	1c4z	A	1239	1565	1.10E-45	0.38	1		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
830	1e0m	A	809	841	2.60E-11	0.06	0.29		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
830	1e0m	A	985	1019	3.90E-12	0.01	0.35		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
832	1alh	A	179	259	3.60E-26	-0.37	0.24		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QGR ZINC FINGER	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) FINGER, DNA-BINDING PROTEIN
832	1alh	A	235	315	2.60E-39	0.04	1		QGR ZINC FINGER	COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
832	1alh	A	263	344	9.10E-38	0.48	1		PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QGSR ZINC FINGER	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
832	1alh	A	598	678	1.40E-30	0.41	0.99		PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QGSR ZINC FINGER	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
832	1alh	A	598	678	3.90E-39	0.27	0.98		PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; QGSR ZINC FINGER	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
832	1mey	C	150	231	3.60E-40	-0.35	0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1mey	C	178	259	1.10E-43	-0.16	0.52		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1mey	C	206	287	3.60E-45	0.1	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1mey	C	234	315	1.60E-46	0.23	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1mey	C	262	343	1.40E-47	0.55	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1mey	C	290	371	1.30E-48	0.49	1		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
	y								CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	318	399	1.80E-49	0.62	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	346	427	1.40E-49	0.34	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	374	455	3.60E-50	0.27	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	402	483	5.40E-50	0.42	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	430	511	7.20E-50	0.16	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	430	538	6.50E-33	-0.22	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	458	539	1.10E-49	0.1	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	514	594	7.20E-48	0.43	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	541	622	1.80E-50	0.69	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	541	623	1.80E-50			101.87	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	569	650	3.60E-50	0.71	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	C	597	678	1.80E-49	0.39	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1me y	G	344	371	1.30E-12	0.06	0.94		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
832	1tf3	A	431	511	1.40E-20	0.15	0.99		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
832	1tf3	A	487	566	3.60E-18	-0.18	0		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
832	1tf6	A	207	352	1.80E-36	0.09	0.84		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
832	1tf6	A	262	431	1.30E-66			105.86	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
832	1tf6	A	263	408	1.60E-36	0.15	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
832	1tf6	A	319	464	3.60E-37	0.32	-1.41		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
832	1tf6	A	431	575	1.30E-36	0.16	-1.41		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
832	1tf6	A	459	603	1.60E-36	-0.05	0.89		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
832	1tf6	A	487	631	1.80E-35	-0.04	0.86		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
832	1tf6	A	515	660	7.20E-35	0.3	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA
832	1ubd	C	158	259	9.00E-29	-0.36	0.18		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	186	287	3.60E-31	-0.38	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	188	315	1.30E-34	-0.37	0.69		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	232	371	2.60E-48	-0.07	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	242	343	3.60E-32	-0.01	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
832	1ubd	C	270	371	1.80E-34	0.23	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	298	399	5.40E-34	0.27	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	344	483	6.50E-52	0.04	0.88		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	354	455	3.60E-34	0.2	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	382	483	7.20E-36	-0.09	0.99		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	410	511	1.40E-34	-0.06	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
832	1ubd	C	428	594	3.90E-42	-0.42	0.53		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	466	566	3.60E-32	0.02	0.34		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	519	622	1.30E-47	0.23	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	522	622	5.40E-36	0.22	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	567	678	5.20E-51	0.43	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	569	679	5.20E-51			86.51	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	577	678	5.40E-34	-0.06	1		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1ubd	C	651	680	2.60E-06	-0.04	0.18		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
832	1zfd		653	680	0.00013	0.15	0.72		SWI5; CHAIN: NULL;	ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTIF, ZINC FINGER DNA BINDING DOMAIN
832	2gli	A	133	317	1.30E-36	-0.16	0.46		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	150	286	1.60E-31	-0.24	0.49		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	208	345	2.60E-52	-0.21	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	235	401	5.20E-63	-0.1	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	262	429	3.90E-64	0.06	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
832	2gli	A	270	398	3.60E-33	0.01	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	318	485	2.60E-64	0.25	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	346	596	3.90E-57	-0.4	0.19		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	354	482	3.60E-34	0.03	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	438	565	1.10E-32	-0.21	0.49		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	459	652	5.20E-60	-0.07	0.19		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	494	624	5.40E-31	-0.02	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	541	678	3.90E-64	0.53	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
832	2gli	A	541	680	3.90E-64			91.33	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
834	1b6g		1240	1332	0.00078	-0.1	0.12		HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
834	1cqw	A	1240	1332	0.0013	-0.19	0.21		HALOALKANE	HYDROLASE A/B HYDROLASE FOLD,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									DEHALOGENASE; 1-CHLOROHEXANE CHAIN: A;	DEHALOGENASE I-S BOND
834	1cvl		1251	1362	0.00026	0.04	0.69		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL-HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
834	1ei9	A	1251	1362	0.00026	-0.1	0.53		PALMITOYL PROTEIN THIOESTERASE I; CHAIN: A;	HYDROLASE ALPHA/BETA
834	1ex9	A	1251	1362	0.00026	0.13	0.46		LACTONIZING LIPASE; CHAIN: A;	HYDROLASE, GLYCOPROTEIN
										HYDROLASE TRIACYLGLYCEROL LIPASE; LIPASE, ALPHA-BETA HYDROLASE FOLD, PSEUDOMONAS, PHOSPHONATE 2 INHIBITOR
836	1ax4	A	13	241	5.40E-07	0.23	0.06		TRYPTOPHANASE; CHAIN: A, B, C, D;	TRYPTOPHAN BIOSYNTHESIS
836	1bj4	A	13	246	7.20E-36	0.08	-0.07		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A;	TRYPTOPHAN BIOSYNTHESIS
836	1c0n	A	2	244	9.00E-41	0.08	-1.41		CSDB PROTEIN; CHAIN: A;	TRYPTOPHAN BIOSYNTHESIS
836	1cj0	A	12	246	7.20E-37	0.05	-0.13		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B;	TRYPTOPHAN BIOSYNTHESIS
836	1cs1	A	4	242	1.60E-31	-0.28	0		HYDROXYMETHYLTRANSFERASE; CHAIN: A, B;	TRYPTOPHAN BIOSYNTHESIS
836	1dfo	A	4	252	3.60E-40	0.17	-1.41		CYSTATHIONINE GAMMA-SYNTHASE; CHAIN: A, B, C, D;	PYRIDOXAL 2 5'-PHOSPHATE, MONOVALENT CATION BINDING SITE
836	1eg5	A	1	248	1.30E-50	0.22	1		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT, SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD
836	1eg5	A	1	248	1.80E-45	0.1	1		AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE PLP-DEPENDENT ENZYMES, IRON-SULFUR-CLUSTER SYNTHESIS, C-S 2 BETA L YASE
836	1eg5	A	1	248	1.80E-45	0.1	1		AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE PLP-DEPENDENT ENZYMES, IRON-SULFUR-CLUSTER SYNTHESIS, C-S 2 BETA L YASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
836	1eji	A	12	246	7.20E-35	0.41	-0.11		SERINE HYDROXYMETHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT, SERINE-GLYCINE CONVERSION, PYRIDOXAL 5'-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER
836	1elu	A	1	241	3.90E-28	-0.03	0.83		L-CYSTEINE/L-CYSTEINE C-S LYASE; CHAIN: A, B;	LYASE FES CLUSTER BIOSYNTHESIS, PYRIDOXAL 5'-PHOSPHATE, 2 THIOCYSTEINE, AMINOACRYLATE, ENZYME-PRODUCT COMPLEX
837	1a3d		131	234	4.80E-39	0.38	-0.08		PHOSPHOLIPASE A2; CHAIN: NULL;	CARBOXYLIC ESTER HYDROLASE PHOSPHOLIPASE, TRIMER, CALCIUM BINDING, ACTIVATOR SITE, 2 CARBOXYLIC ESTER HYDROLASE
837	1ae7		131	244	4.80E-41	0.07	-0.18		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE PLA2, PHOSPHATIDE SN-2 ACYLHYDROLASE;
837	1bk9		131	253	1.60E-40	0.07	-0.13		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE, PHOSPHOLIPASE A2, LIPID DEGRADATION, PRESYNAPTIC 2 NEUROTOXIN, VENOM
837	1poa		131	234	1.60E-38	0.3	-0.14		HYDROLASE PHOSPHOLIPASE A2 (E.C.3.1.1.4) IPOA 3	HYDROLASE HYDROLASE, PHOSPHOLIPASE A2, PLATELET AGGREGATION INHIBITOR, 2 PBPB HEADER MODRES
837	1poc		151	289	1.40E-36			99.59	HYDROLASE PHOSPHOLIPASE A2 (E.C.3.1.1.4) COMPLEX WITH THE IPOC 3 TRANSITION-STATE ANALOGUE IPOC 4	
837	1poc		355	438	0.0054	0.08	0.21		HYDROLASE PHOSPHOLIPASE A2 (E.C.3.1.1.4) COMPLEX WITH THE IPOC 3 TRANSITION-STATE ANALOGUE IPOC 4	
837	1pp2	R	131	253	1.60E-38	0.2	-0.14		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A2=(E.C.3.1.1.4) IPP2 4	
837	1vap	A	131	253	3.20E-44	0.12	-0.17		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
837	1vip		131	248	4.80E-41	0.15	-0.11		PHOSPHOLIPASE A2; CHAIN: NULL;	DEGRADATION, HYDROLASE HYDROLASE HYDROLASE, PHOSPHOLIPASE A2, ANTICOAGULANT
837	2not	A	131	244	1.30E-40	0.4	-0.08		PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE HYDROLASE, LIPID DEGRADATION, CALCIUM, PRESYNAPTIC 2 NEUROTOXIN, VENOM
837	3p2p	A	132	236	1.60E-38	0.34	-0.06		HYDROLASE(CARBOXYL ESTER) PHOSPHOLIPASE A=2= (PHOSPHATIDE-2-ACYL-HYDROLASE) MUTANT 3P2P 4 WITH ASP 59 REPLACED BY SER, SER 60 REPLACED BY GLY, 3P2P 5 62-66 DELETED, ASN 67 REPLACED BY TYR 3P2P 6 (D59SS, /S60GS, DEL(62-66), /N67YS) (E.C.3.1.1.4) 3P2P 7	
838	1b8q	A	21	106	1.30E-13	0.79	0.98		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
838	1be9	A	12	102	1.10E-18	0.21	0.72		PSD-95; CHAIN: A; CRIP1; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
838	1be9	A	254	317	6.40E-10	-0.25	0.1		PSD-95; CHAIN: A; CRIP1; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
838	1i16		21	109	7.20E-16	0.59	0.99		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CEMOATTRACTANT FACTOR, PDZ DOMAIN
838	1i16		4	108	1.40E-14	-0.03	0.45		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CEMOATTRACTANT FACTOR, PDZ DOMAIN
838	1kwa	A	21	108	1.30E-14	0.04	0.66		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
838	1pdr		20	113	6.40E-17	0.45	0.88		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
838	1qau	A	21	106	9.00E-15	-0.12	0.57		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	TRANSDUCTION, SH3 DOMAIN, REPEAT OXIDOREDUCTASE BETA-FINGER
838	1qav	A	20	103	3.20E-17	0.49	0.86		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
838	1qlc	A	20	107	1.40E-18	0.28	1		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
838	3pdz	A	23	99	6.40E-17	-0.09	0.45		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING
840	1bg6		481	594	1.60E-05	-0.18	0.17		N-(1-D-CARBOXYETHYL)-L-NORVALINE DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE (D, L) STEREOSPECIFIC OPINE DEHYDROGENASE, OXIDOREDUCTASE
840	1cf2	P	480	570	0.0069	-0.1	0.09		GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE; CHAIN: P, R, O, Q;	OXIDOREDUCTASE OXYDOREDUCTASE
840	1eyz	A	482	599	0.0054	-0.09	0.05		PHOSPHORIBOSYLGLYCINA MIDE FORMYLTRANSFERASE 2; CHAIN: A, B;	TRANSFERASE TRANSFORMYLASE, PURINE BIOSYNTHESIS, ATP-GRASP
840	1ff9	A	481	924	4.80E-58	1.04	1		SACCHAROPINE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE LYSINE BIOSYNTHESIS, ALPHA-AMINOADIPATE PATHWAY, 2 SACCHAROPINE REDUCTASE, DEHYDROGENASE
840	1pic	A	25	460	1.30E-61	-0.24	0.49		L-ALANINE DEHYDROGENASE; CHAIN: A;	OXIDOREDUCTASE OXIDOREDUCTASE, NAD
842	1bm _p		112	213	9.60E-48	0.14	1		BONE MORPHOGENETIC PROTEIN-7; CHAIN: NULL;	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
842	1bm p		112	214	9.60E-48			104.28	BONE MORPHOGENETIC PROTEIN-7; CHAIN: NULL;	BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
842	2igi		100	214	1.80E-38			67.81	GROWTH FACTOR TRANSFORMING GROWTH FACTOR-BETA TWO (TGF-B2) 2TGI 3	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
842	2igi		102	213	1.60E-36	0.04	0.81		GROWTH FACTOR TRANSFORMING GROWTH FACTOR-BETA TWO (TGF-B2) 2TGI 3	
842	2igi		112	213	1.80E-38	0.11	0.6		GROWTH FACTOR TRANSFORMING GROWTH FACTOR-BETA TWO (TGF-B2) 2TGI 3	
842	3bm p	A	111	213	4.80E-48	0.05	1		BONE MORPHOGENETIC PROTEIN 2 (BMP-2); CHAIN: A;	CYTOKINE CYTOKINE, BONE MORPHOGENETIC PROTEIN, CYSTIN-KNOT, TGFB-2 FAMILY
843	1al7		430	605	0.00013	0.16	0.25		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
843	1al7		665	805	1.60E-07	0.23	0.11		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
843	1al7		992	1103	1.40E-05	0.47	0.8		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
843	lawo		193	242	1.30E-06	0.22	0.66		ABL TYROSINE KINASE; CHAIN: NULL;	KINASE KINASE, SH3 DOMAIN, TRANSFERASE, PHOSPHOTRANSFERASE, 2 PROTO-ONCOGENE, MULTIPLE DOMAIN, LEUKEMIA
843	lefn	A	193	242	7.20E-08	0.46	0.19		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN; CHAIN: B, D;	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTIF
843	lelr	A	432	594	1.10E-05	0.32	0.57		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
843	lelr	A	452	526	9.60E-08	0.11	0.06		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
843	lelr	A	720	815	8.00E-08	-0.02	0.04		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
843	lelr	A	783	899	3.20E-10	-0.08	0.22		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
843	lelw	A	1000	1119	6.40E-11	0.02	-0.08		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
843	lelw	A	441	575	0.00014	0.24	0.09		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
843	lelw	A	742	873	1.10E-06	0.33	0.06		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
843	lfeh	A	375	601	9.00E-07	0.22	0.75		PEROXISOMAL TARGETING SIGNAL, 1 RECEPTOR;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
843	1fch	A	445	804	3.60E-09	0.29	0.62		CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D; PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
843	1fch	A	452	699	1.30E-20	0.06	-0.15		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
843	1fch	A	576	842	1.10E-12	0.02	0.99		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
843	1fyn	A	193	242	1.80E-07	0.23	0.4		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN. 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
843	lgr	A	181	249	1.40E-06	0.74	0.59		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
843	lck	A	193	288	1.80E-05	0.09	0.28		P56 ^{lck} =LCK=TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL	COMPLEX (KINASE/PEPTIDE)
843	lnlo	C	193	242	1.80E-07	0.4	0.29		TEGQ(PHOSPHO)YQPQA; ILCK 14 CHAIN: B; ILCK 15 C-SRC; CHAIN: C; NLI (MN7-	COMPLEX (TRANSFERASE/PEPTIDE)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
843	1pnj		182	249	9.00E-10	0.54	0.17		MN2-MN1-PLPPLP); CHAIN: N;	SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
843	1qcf	A	193	282	3.60E-07	0.09	0.17		PHOSPHOTRANSFERASE PHOSPHATIDYLINOSITOL 3-KINASE (P85-ALPHA SUBUNIT, IPNJ 3 SH3 DOMAIN) (NMR, MINIMIZED AVERAGE STRUCTURE) IPNJ 4	
843	1qqe	A	418	573	1.80E-07	0.06	0.15		HAEMATOPOIETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
843	1qqe	A	949	1101	8.00E-06	-0.03	0.09		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
843	1shf	A	188	242	9.00E-08	0.38	0.54		VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	PROTEIN TRANSPORT HELIX-TURN-HELIX TPR-LIKE REPEAT, PROTEIN TRANSPORT
843	4hck		193	255	9.00E-06	0.45	0.89		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
846	1.20 E+09	H	236	414	6.40E-51	0.08	-0.06		HAEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
846	1ae6	H	419	599	4.80E-53	-0.18	0.03		2E8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
846	1afv	H	21	220	4.80E-63	0.05	0.24		ANTIBODY CTM01; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
									HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB253 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
846	1b1h	A	134	503	5.40E-62			159.92	HEMOLIN; CHAIN: A, B;	CAPSID PROTEIN, 2 P24 INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
846	1b1h	A	135	503	5.40E-62	0.28	1		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
846	1b1h	A	138	493	1.60E-31	0.29	0.54		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
846	1b1h	A	27	404	7.20E-48	0.15	0.66		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
846	1b1h	A	323	713	3.20E-22	0.14	0.21		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
846	1b1j		508	597	1.40E-12	0.07	-0.05		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
846	1b1n	B	21	220	3.20E-64	0.36	0.04		MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM
846	1c1c	B	235	412	1.60E-49	0.17	-0.13		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB COMPLEX, IDIOTOPE, ANTI-IDIOPE
846	1c17	I	523	603	6.40E-23	0.03	-0.19		IGG1 ANTIBODY 1696 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 1696 (VARIABLE HEAVY CHAIN); CHAIN: H; IGG1 ANTIBODY 1696 (CONSTANT HEAVY CHAIN); CHAIN: I;	IMMUNE SYSTEM IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1 FAB FRAGMENT, CROSS-REACTIVITY, HIV1 PROTEASE, ENZYME 2 INHIBITION, IMMUNOGLOBULIN
846	1c19	H	236	415	3.20E-49	0.06	-0.11		FAB ANTIBODY LIGHT	IMMUNE SYSTEM ANTI-PRION FAB

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
									CHAIN: L; FAB ANTIBODY HEAVY CHAIN; CHAIN: H;	3F4; ANTI-PRION FAB 3F4 ANTI-PRION ANTIBODY, FAB 3F4
846	1cs6	A	135	503	3.60E-59	0.08	1		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
846	1cs6	A	138	503	4.80E-45	0.24	1		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
846	1cs6	A	2	321	1.60E-47	-0.14	0.43		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
846	1cs6	A	20	412	1.10E-37	0.02	-0.14		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
846	1cs6	A	226	592	1.80E-44	0.23	0.96		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
846	1cs6	A	236	602	6.40E-42	0.13	1		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
846	1cs6	A	24	404	1.60E-53	0.07	0.58		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
846	1cs6	A	320	713	3.20E-33	0.07	0.51		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
846	1cvs	C	135	320	1.80E-30	0.15	0.94		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
846	1cvs	C	430	601	3.20E-21	0.07	0.22		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
846	1cvs	D	135	320	1.80E-32	0.22	0.99		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
846	1cvs	D	430	601	8.00E-21	0.26	-0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
846	1dgi	R	141	404	7.20E-36	-0.3	0.65		CHAIN: C, D; POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
846	1dgi	R	228	503	1.10E-38	-0.31	0.21		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	
846	1dgi	R	28	319	3.60E-44	-0.4	0.01		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	
846	1dn2	A	234	411	8.00E-40	-0.27	0.05		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F; IGM MEZ	
846	1dql	H	21	130	3.20E-38	0.09	-0.09		IMMUNOGLOBULIN; CHAIN: L, IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
846	1dzb	A	21	206	6.40E-42	0.14	-0.03		SCFV FRAGMENT 1F9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N-ACETYLMURAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT
846	1epf	A	142	319	1.80E-31	0.34	0.9		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
846	1epf	A	324	503	1.30E-24	0.37	0.78		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
846	1ev2	E	135	320	1.40E-34	0.07	0.96		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG) LIKE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
846	1ev2	E	33	224	7.20E-23	0.15	0.17		FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
846	1ev2	G	135	322	5.40E-33	0.23	0.94		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
846	1ev2	G	329	505	3.60E-24	0.27	0.94		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
846	1ev2	G	430	601	1.60E-19	0.15	0.07		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
846	1evt	C	135	320	1.30E-30	0.11	0.69		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
846	1evt	C	430	601	6.40E-20	-0.07	0.07		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
846	1f2q	A	136	322	7.20E-28	0.09	0.29		HIGH AFFINITY IMMUNOGLOBULIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
846	1f4w	H	21	220	1.60E-62	0.02	0		EPSILON RECEPTOR CHAIN: A;	GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
846	1f6a	A	132	322	1.10E-29	0.17	0.18		ANTIBODY S-20-4, FAB FRAGMENT, LIGHT CHAIN; CHAIN: L; ANTIBODY S-20-4, FAB FRAGMENT, HEAVY CHAIN; CHAIN: H	IMMUNE SYSTEM ANTI-CARBOHYDRATE ANTIBODY
846	1f6f	B	524	715	9.00E-15	0.05	0.03		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
846	1f62	D	234	411	1.10E-39	-0.03	0.07		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
846	1f6g	A	143	319	1.10E-24	-0.16	0.23		IMMUNOGLOBULIN IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
846	1f6h	A	512	708	3.60E-17	0.17	0.52		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
846	1f6l	A	139	319	1.80E-22	-0.02	0.36		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
846	1hmf		141	305	1.60E-21	-0.31	0.04		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
846	1hng	A	143	319	3.60E-27	0.03	0.05		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (HUMAN) IHN3	
846	1igt	B	21	412	0	-0.16	0.11		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) IHNG 3	
846									IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
846	1igy	B	13	412	3.20E-95			110.16	IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	REGION, IMMUNOGLOBULIN
846	1igy	B	21	411	3.20E-95	-0.05	0.24		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
846	1itb	B	225	503	5.40E-29	0.21	0.49		INTERLEUKIN-1 BETA; CHAIN: A; TYPE I INTERLEUKIN-1 RECEPTOR; CHAIN: B;	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
846	1kb5	H	235	413	1.10E-49	0.11	-0.17		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
846	1lmk	A	21	206	3.20E-39	-0.23	0.01		IMMUNOGLOBULIN ANTI- PHOSPHATIDYLINOSITOL SPECIFIC PHOSPHOLIPASE C DIABODY 1LMK 3 SYNONYMS: L5MK16 DIABODY, SINGLE-CHAIN FV DIMER 1LMK 4	
846	1ma m	H	21	220	4.80E-62	-0.05	0.22		IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT (FAB) (IGG2B, KAPPA) IMAM 3	
846	1mc o	H	20	411	1.60E-93	-0.17	0.04		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
846	1mc o	H	24	416	1.60E-93			123.28	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
846	1mc p	H	21	210	8.00E-46	-0.26	0.06		IMMUNOGLOBULIN IMMUNOGLOBULIN FAB FRAGMENT (MCP/PC\$603)	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
846	1mfn		512	715	3.60E-21	-0.03	0.15		IMCP 4	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
846	1mrd	H	21	220	9.60E-64	0.05	-0.06		IMMUNOGLOBULIN IGG JEL 103 FAB FRAGMENT COMPLEXED WITH 1MRD 3 INOSINE-5'-DIPHOSPHATE 1MRD 4	
846	1mfd	F	21	220	4.80E-62	0.05	-0.05		N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
846	1ngp	H	21	220	1.60E-63	0.14	0.13		N1G9 (IGG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN
846	1nqb	A	21	206	3.20E-43	-0.11	0.04		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	IMMUNOGLOBULIN VARIABLE HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
846	1qg3	A	449	599	5.40E-15	0.08	0.21		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
846	1qg3	A	508	715	1.80E-23	0.1	0.24		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
846	1qkz	H	21	220	3.20E-63	0.12	-0.01		ANTIBODY; CHAIN: H, L; PROTEIN G-PRIME; CHAIN: A; MAJOR OUTER MEMBRANE PROTEIN P1.16; CHAIN: P;	IMMUNE SYSTEM FAB, PORA, NEISSERIA MENINGITIDIS, PORIN
846	1qkq	A	21	211	8.00E-40	0.24	0.25		MFE-23 RECOMBINANT ANTIBODY FRAGMENT; CHAIN: A;	IMMUNOGLOBULIN IMMUNOGLOBULIN, SINGLE-CHAIN FV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN
846	1qr4	A	512	713	5.40E-19	0.04	0.19		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
										FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
846	1vca	A	137	319	3.60E-24	0.19	0.74		HUMAN VASCULAR CELL ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	CELL ADHESION PROTEIN VCAM-D1,2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15
846	1wej	H	236	413	8.00E-50	0.09	-0.14		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
846	1yuh	H	419	602	8.00E-53	0	-0.15		FAB FRAGMENT; CHAIN: NULL;	IMMUNOGLOBULIN ANTI-NITROPHENOL, LAMBDA LIGHT CHAIN, IMMUNOGLOBULIN
846	1zxq		135	326	1.80E-34	0	0.09		INTERCELLULAR ADHESION MOLECULE-2; CHAIN: NULL;	CELL ADHESION ICAM-2; IMMUNOGLOBULIN FOLD, CELL ADHESION, GLYCOPROTEIN, 2 TRANSMEMBRANE, REPEAT, SIGNAL
846	2dli	A	134	320	7.20E-28	0.29	0.09		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
846	2fbj	H	21	210	3.20E-50	0.12	0.19		IMMUNOGLOBULIN IG*A FAB FRAGMENT (J539) (GALACTAN-BINDING) 2FBJ 3	
846	2fcb	A	135	323	7.20E-36	0.13	0.81		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
846	2fcb	A	226	410	9.00E-29	-0.04	0.21		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
846	8fab	A	234	407	9.60E-28	-0.35	0		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
847	1dn1	B	299	480	1.60E-09	0.05	0.11		SYNTAXIN BINDING PROTEIN 1; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									SYNTAXIN 1A; CHAIN: B;	MULTI-SUBUNIT
848	1d2k	A	2	297	4.80E-63	0.35	1		CHITINASE 1; CHAIN: A;	HYDROLASE BETA-ALPHA BARREL
848	1dqc	A	323	367	1.60E-10	0.19	-0.09		TACHYCITIN; CHAIN: A	ANTIMICROBIAL PROTEIN DISULFIDE-RICH
848	1.00 E+15	A	1	265	1.10E-81	0.47	1		CHITINASE B; CHAIN: A, B;	HYDROLASE HYDROLASE, CHITIN DEGRADATION
848	1.00 E+15	A	2	266	1.60E-59	0.51	1		CHITINASE B; CHAIN: A, B;	HYDROLASE HYDROLASE, CHITIN DEGRADATION
848	1edq	A	1	281	3.60E-79	0.41	1		CHITINASE A; CHAIN: A;	HYDROLASE BETA-ALPHA (TIM)
848	1edq	A	4	260	9.60E-70	0.33	1		CHITINASE A; CHAIN: A;	BARREL
848	1edt		4	146	4.80E-05	-0.15	0.13		HYDROLASE (GLUCOSIDASE) ENDO- BETA-N- ACETYLGLUCOSAMINIDAS E H, ENDO H (E.C.3.2.1.96) 1EDT 3	HYDROLASE BETA-ALPHA (TIM)
848	2ebn		1	204	7.20E-51	0.25	0.06		HYDROLASE(GLUCOSIDASE) ENDO-BETA-N- ACETYLGLUCOSAMINIDAS E F1 (E.C.3.2.1.96) 2EBN 3 (ENDOGLYCOSIDASE F1, ENDO F1) 2EBN 4	BARREL
848	2ebn		4	111	0.0067	-0.3	0.77		HYDROLASE(GLUCOSIDASE) ENDO-BETA-N- ACETYLGLUCOSAMINIDAS E F1 (E.C.3.2.1.96) 2EBN 3 (ENDOGLYCOSIDASE F1, ENDO F1) 2EBN 4	BARREL
849	1ahd	P	284	351	7.20E-33			77.33	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
849	1ahd	P	286	337	6.40E-29	0.13	1		DNA-BINDING PROTEIN	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
849	1ahd	P	286	351	7.20E-33	-0.38	1		ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
849	1b72	A	274	346	5.40E-32			62.11	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
849	1b72	A	286	346	5.40E-32	-0.08	1		HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
849	1b8i	A	285	342	5.40E-31			65.54	ULTRABITHORAX HOMEOBOX PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D; ULTRABITHORAX	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOBOX PROTEINS, DEVELOPMENT, 2 SPECIFICITY
849	1b8i	A	286	342	5.40E-31	-0.11	0.99		HOMEOBOX PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D; ULTRABITHORAX	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOBOX PROTEINS, DEVELOPMENT, 2 SPECIFICITY
849	1d0s	A	35	238	7.20E-11	0.15	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
849	1ftz		283	351	1.30E-27			68.94	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
849	1ftz		284	337	1.30E-27	-0.31	0.84		STRUCTURES IFTZ 3 DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
849	l-Oct	C	205	344	7.20E-34	-0.2	0.12		DNA-BINDING PROTEIN OCT-1 (POU DOMAIN) OCT 3	
849	lsan		290	351	5.40E-30			72.13	DNA-BINDING PROTEIN ANTENNAPEPIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
849	lsan		291	337	1.40E-26	-0.21	1		DNA-BINDING PROTEIN ANTENNAPEPIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
849	lsan		292	351	5.40E-30	-0.2	1		DNA-BINDING PROTEIN ANTENNAPEPIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	
849	9ant	A	289	337	1.30E-27	0.11	1		ANTENNAPEPIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
849	9ant	A	289	344	9.00E-30			69.06	ANTENNAPEPIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
849	9ant	A	289	344	9.00E-30	0.27	1		ANTENNAPEPIA PROTEIN;	COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A, B; DNA; CHAIN: C, D, E, F;	PROTEIN/DNA HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)
851	1a6a	B	33	157	3.20E-66			54.43	HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
851	1a6a	B	34	147	3.20E-66	-0.32	0.93		HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
851	1a6d	B	33	147	6.40E-69	-0.33	0.63		HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, I, K; HLA-A2; CHAIN: C, F, I, L;	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN
851	1a6d	B	33	157	6.40E-69			55.9	HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, I, K; HLA-A2; CHAIN: C, F, I, L;	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN
851	1bx2	B	32	147	1.60E-69	-0.22	0.87		HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
851	1bx2	B	32	157	1.60E-69			52.4	HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
851	1d5m	B	31	147	4.80E-62	-0.33	0.92		HLA CLASS II HISTOCOMPATIBILITY ANTIGEN; CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN; CHAIN: B; ENTEROTOXIN TYPE B; CHAIN: C; PEPTIDE INHIBITOR; CHAIN: D;	IMMUNE SYSTEM HLA-DR4; HLA-DR4; SEB, SUPERANTIGEN; COMPLEX (MHC CLASS II/SUPERANTIGEN), IMMUNE SYSTEM
851	1fv1	B	30	147	3.20E-67	-0.31	0.82		MAJOR HISTOCOMPATIBILITY	IMMUNE SYSTEM MHC CLASS II DR2A

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN: B, E; MYELIN BASIC PROTEIN; CHAIN: C, F;	
851	1iak	B	36	147	4.80E-53	-0.4	0.46		MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
851	1iao	B	23	157	9.60E-57			52.61	MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC, I-A, OVALBUMIN PEPTIDE
851	1iao	B	35	147	9.60E-57	-0.39	0.71		MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC, I-A, OVALBUMIN PEPTIDE
851	1iea	B	29	147	1.40E-63	-0.27	0.9		MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC II MHC II, CLASS II MHC, I-A, OVALBUMIN PEPTIDE
851	1iea	B	8	157	1.40E-63			50.29	MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
851	1ieb	B	24	147	8.00E-64	-0.43	0.87		MHC CLASS II I-EK; CHAIN: A, B, C, D;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
851	2iad	B	22	157	3.20E-58			52.73	MHC CLASS II I-AD; CHAIN: A, B;	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN
851	2iad	B	26	147	3.20E-58	-0.5	1		MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC I-AD MHC II MHC II, CLASS II MHC I-AD
856	1bf9		443	474	0.0072	-0.42	0.17		FACTOR VII; CHAIN: NULL;	BLOOD COAGULATION BLOOD COAGULATION, EGF, HYDROLASE, SERINE PROTEASE
856	1cwv	A	2	229	3.60E-19	0.05	-0.19		INVASIN; CHAIN: A;	STRUCTURAL PROTEIN INTEGRIN- BINDING PROTEIN, INV GENE
856	1cyg		17	226	7.20E-15	0.07	-0.19		GLYCOSYLTRANSFERASE CYCLODEXTRIN GLUCANOTRANSFERASE (E.C.2.4.1.19) (CGTASE) ICYG 3	
856	1dan	L	404	475	0.009	-0.24	0.04		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE- ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
856	1dva	L	429	472	0.0036	0.07	0.28		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H; I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L; M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
856	1eut		18	232	7.20E-13	0.22	-0.19		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
856	177e	A	443	475	0.0036	-0.28	0.11		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING
856	1hae		429	482	0.0072	-0.21	0		HEREGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
856	1hre		230	254	0.0072	-0.7	0.23		GROWTH FACTOR (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) IHRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IHRE 4	
856	1pam	A	1	171	5.40E-12	0.04	-0.19		CYCLODEXTRIN GLUCANOTRANSFERASE; CHAIN: A, B;	GLYCOSYLTRANSFERASE TRANSFERASE, GLYCOSYLTRANSFERASE, CALCIUM, SIGNAL
857	1bu8	A	18	256	3.60E-83	0.85	1		PANCREATIC LIPASE RELATED PROTEIN 2; CHAIN: A;	HYDROLASE HYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE
857	1bu8	A	18	276	4.80E-65	0.81	1		PANCREATIC LIPASE RELATED PROTEIN 2; CHAIN: A;	HYDROLASE HYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE
857	1eth	A	18	276	1.60E-66			167.54	TRIACYLGLYCEROL ACYL-HYDROLASE; CHAIN: A, C; COLIPASE; CHAIN: B, D	COMPLEX (HYDROLASE/COFACTOR) TRIACYLGLYCEROL LIPASE; COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION
857	1eth	A	18	276	1.60E-66	0.65	1		TRIACYLGLYCEROL ACYL-HYDROLASE; CHAIN: A, C; COLIPASE; CHAIN: B, D	COMPLEX (HYDROLASE/COFACTOR) TRIACYLGLYCEROL LIPASE; COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
857	1gpl		18	276	1.80E-80			176.81	RP2 LIPASE; CHAIN: NULL;	SERINE ESTERASE RELATED PROTEIN 2 LIPASE; SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC
857	1gpl		19	256	1.80E-80	0.87	1		RP2 LIPASE; CHAIN: NULL;	SERINE ESTERASE RELATED PROTEIN 2 LIPASE; SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC
857	1gpl		19	276	3.20E-65	0.76	1		RP2 LIPASE; CHAIN: NULL;	SERINE ESTERASE RELATED PROTEIN 2 LIPASE; SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC
857	1hpl	A	18	274	1.60E-76			167	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) (TRIACYLGLYCEROL HYDROLASE) ILPB 3	
857	1lpb	B	18	256	1.10E-79	0.83	1		HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
857	1lpb	B	18	276	1.10E-79			173.41	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
857	1lpb	B	18	276	1.60E-65	0.81	1		HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
857	1rp1		18	257	5.40E-83	0.69	1		UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
857	1rp1		18	274	5.40E-83			183.05	PANCREATIC LIPASE RELATED PROTEIN 1; CHAIN: NULL;	HYDROLASE HYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE
857	1rp1		18	276	1.60E-63	0.71	1		PANCREATIC LIPASE RELATED PROTEIN 1; CHAIN: NULL;	HYDROLASE HYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE
859	1dn1	B	14	156	0.00036	-0.08	0		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B; TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
859	1ej	A	151	308	1.30E-44	0.28	0.07			TRANSCRIPTION INHIBITOR BETA-PROPELLER
859	1got	B	132	298	8.00E-46	0.19	0.12		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
859	1got	B	8	309	1.10E-40			52.34	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
859	1got	B	95	309	1.10E-40	0.13	-0.11		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
859	1qks	A	221	304	1.30E-14	0	-0.12		CYTOCHROME CD1 NITRITE REDUCTASE; CHAIN: A, B;	HETEROTRIMER 2 SIGNAL TRANSDUCTION OXIDOREDUCTASE ENZYME, NITRITE REDUCTASE, OXIDOREDUCTASE, DENITRIFICATION, 2 ELECTRON TRANSPORT, PERIPLASMIC
860	1alh	A	141	221	1.60E-25	-0.3	0.15		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
860	1alh	A	197	277	1.80E-39	0.04	1		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
860	1alh	A	225	306	9.00E-38	0.48	1		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
860	1alh	A	560	640	3.60E-39	0.27	0.98		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
860	1alh	A	560	640	6.40E-31	0.41	0.99		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
860	1mey	C	112	193	1.10E-39	-0.35	0.07		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1mey	C	140	221	3.20E-43	-0.16	0.52		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1mey	C	168	249	1.40E-44	0.1	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
860	1mey	C	196	277	1.60E-46	0.23	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1mey	C	224	305	1.60E-47	0.55	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1mey	C	252	333	1.40E-48	0.49	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1mey	C	280	361	3.20E-49	0.62	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1mey	C	308	389	8.00E-50	0.34	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1mey	C	336	417	1.60E-50	0.27	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1mey	C	364	445	1.60E-50	0.42	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1mey	C	392	473	4.80E-50	0.16	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
860	1me y	C	392	500	7.20E-33	-0.22	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1me y	C	420	501	9.60E-50	0.1	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1me y	C	448	528	3.20E-47	0.15	0.96		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1me y	C	476	556	3.20E-47	0.43	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1me y	C	503	584	9.60E-50	0.69	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1me y	C	503	585	8.00E-50			101.87	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1me y	C	531	612	8.00E-50	0.71	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1me y	C	559	640	1.60E-49	0.39	1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI- BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
860	1me y	G	306	333	3.60E-14	0.06	0.94		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1me y	G	306	333	4.80E-13	0.06	0.94		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
860	1tf6	A	113	258	4.80E-31	-0.25	0.12		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
860	1tf6	A	169	314	1.60E-35	0.11	0.99		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
860	1tf6	A	224	393	1.80E-66			105.92	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
860	1tf6	A	225	370	4.80E-37	0.21	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
860	1tf6	A	281	426	1.60E-38	0.32	1		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
860	1tf6	A	393	537	1.30E-36	0.16	0.99		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

[illegible]

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Coumpound	PDB annotation
860	1ubd	C	170	277	3.20E-32	-0.19	0.93		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	194	333	1.80E-48	-0.07	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	227	333	4.80E-34	0.19	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	260	361	3.20E-34	0.27	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	306	445	5.40E-52	0.04	0.88		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	316	417	3.20E-34	0.2	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	372	473	4.80E-35	-0.14	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	390	556	3.60E-42	-0.42	0.53		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	400	501	6.40E-35	0	0.78		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	456	556	3.20E-31	-0.07	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	481	584	1.80E-47	0.23	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	484	584	3.20E-36	0.22	1		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
860	1ubd	C	529	640	5.40E-51	0.43	0.98		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	531	641	5.40E-51			86.51	YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1ubd	C	539	640	3.20E-34	-0.06	1		YY1; CHAIN: C; ADENOVIRUS P5 ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
860	1zfd		615	642	0.00016	0.15	0.72		SWI5; CHAIN: NULL;	TRANSCRIPTION REGULATION/DNA
860	2gli	A	140	276	3.20E-31	-0.04	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTIF, ZINC FINGER DNA BINDING DOMAIN
860	2gli	A	170	307	3.60E-52	-0.21	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
860	2gli	A	197	363	5.40E-63	-0.1	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
860	2gli	A	224	391	3.60E-64	0.06	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	227	360	1.60E-33	0.13	0.98		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	280	447	1.80E-64	0.25	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	308	558	3.60E-57	-0.4	0.19		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	316	444	1.30E-34	0.03	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	400	527	1.60E-32	-0.21	0.49		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	421	614	5.40E-60	-0.07	0.19		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	456	586	1.30E-30	-0.02	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	484	611	1.40E-35	0.27	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	503	640	3.60E-64	0.33	1		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
860	2gli	A	503	642	3.60E-64			91.33	ZINC FINGER PROTEIN GLI1;	COMPLEX (DNA-BINDING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
860	2gli	A	95	279	1.40E-36	-0.16	0.46		ZINC FINGER PROTEIN GLI;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
862	1din		255	338	0.00013	0.02	0.96		DIENELACTONE HYDROLASE; CHAIN: NULL;	HYDROLYTIC ENZYME DLH; DIENELACTONE HYDROLASE, AROMATIC HYDROCARBON CATABOLISM, 2 SERINE ESTERASE, CARBOXYMETHYLENEBUTENOLIDE, 3 HYDROLYTIC ENZYME
864	1aip	C	2646	2676	0.00018	0.02	0.66		ELONGATION FACTOR TU; CHAIN: A, B, E, F; ELONGATION FACTOR TS; CHAIN: C, D, G, H;	COMPLEX OF TWO ELONGATION FACTORS EF-TU; EF-TS; ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP-BINDING 2 COMPLEX OF TWO ELONGATION FACTORS
864	1eft	B	2646	2673	0.00018	-0.56	0.75		ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)
865	1aab		106	185	9.00E-18	-0.09	0.89		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
865	1aab		363	433	5.40E-16	0.68	1		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
865	1aab		528	590	1.80E-06	0.41	0.33		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
865	1cg7	A	112	180	1.80E-16	-0.12	0.94		NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMG BOX, DNA BINDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
865	1cg7	A	262	320	3.60E-07	0.3	0.83		NON HISTONE PROTEIN 6 A; CHAIN: A;	PROTEIN DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
865	1cg7	A	369	433	5.40E-16	0.45	1		NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
865	1cg7	A	476	516	7.20E-06	-0.4	0.42		NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
865	1cg7	A	532	601	1.80E-06	0.28	0.24		NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
865	1ckt	A	112	177	5.40E-14	-0.29	0.92		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'- D(*CP*CP*(IDO) CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
865	1ckt	A	262	320	3.60E-07	0.02	0.71		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'- D(*CP*CP*(IDO) CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
865	1ckt	A	369	433	3.60E-15	0.4	0.99		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'- D(*CP*CP*(IDO) CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
865	1ckt	A	476	510	7.20E-05	0.03	0.11		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'- D(*CP*CP*(IDO) CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
865	1ckt	A	530	590	1.40E-05	-0.01	0.01		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-D*CP*CP*(IDO) CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
865	1cun	A	382	585	7.20E-08	-0.16	0		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
865	1hmc		107	160	3.60E-14	0	0.57		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING IHME 3 HMG-BOX DOMAIN B OF RAT HMGI) (NMR, 1 STRUCTURE) IHME 4	
865	1hme		257	303	0.00036	-0.19	0.43		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING IHME 3 HMG-BOX DOMAIN B OF RAT HMGI) (NMR, 1 STRUCTURE) IHME 4	
865	1hme		369	418	3.60E-13	0.04	1		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING IHME 3 HMG-BOX DOMAIN B OF RAT HMGI) (NMR, 1 STRUCTURE) IHME 4	
865	1hry	A	110	180	9.00E-15	-0.52	0.39		HUMAN SRV; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: B; IHRY 10	COMPLEX (DNA-BINDING PROTEIN/DNA)
865	1hry	A	368	433	1.80E-16	0.19	0.78		HUMAN SRV; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: B; IHRY 10	COMPLEX (DNA-BINDING PROTEIN/DNA)
865	1hsm		112	160	9.00E-12	0.44	0.21		DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMGI) BOX 2,	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
865	1hsm		262	303	0.00036	0.02	0.37		COMPLEXED WITH IHSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) IHSM 4 DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH IHSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) IHSM 4	
865	1hsm		369	418	5.40E-13	0.6	1		DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH IHSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) IHSM 4	
865	1qrv	A	112	153	1.10E-10	-0.69	0.01		DNA (5'-D(*GP*CP*GP*AP*TP*AP*TP*CP*GP*C)-3'); CHAIN: C, D; HIGH MOBILITY GROUP PROTEIN D; CHAIN: A, B;	GENE REGULATION/DNA HMG-D; PROTEIN-DNA COMPLEX, HMG DOMAIN, NON-SEQUENCE SPECIFIC 2 CHROMOSOMAL PROTEIN HMG-D
865	1qrv	A	367	411	5.40E-12	0.18	0.78		DNA (5'-D(*GP*CP*GP*AP*TP*AP*TP*CP*GP*C)-3'); CHAIN: C, D; HIGH MOBILITY GROUP PROTEIN D; CHAIN: A, B;	GENE REGULATION/DNA HMG-D; PROTEIN-DNA COMPLEX, HMG DOMAIN, NON-SEQUENCE SPECIFIC 2 CHROMOSOMAL PROTEIN HMG-D
865	2lef	A	113	180	1.80E-14	-0.23	0.36		LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
865	2lef	A	262	320	3.60E-07	0.11	0.58		LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
865	2lef	A	371	433	1.10E-14	0.76	1		LYMPHOID ENHANCER-	GENE REGULATION/DNA LEF-1 HMG;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									BINDING FACTOR; CHAIN: A; DNA (5'-CHAIN: B; DNA (5'-CHAIN: C;	LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
865	2lef	A	532	590	3.60E-06	0.28	0.68		LYMPHOID ENHANCER-BINDING FACTOR; CHAIN: A; DNA (5'-CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
865	2irc	P	639	709	3.60E-12	0.78	-0.19		TRANSDUCIN; CHAIN: B; G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, 3 G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
866	1ez3	A	396	465	1.80E-09	0.53	-0.2		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
866	1quu	A	396	467	5.40E-09	0.58	-0.19		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
866	1req	A	390	464	3.60E-12	0.36	-0.2		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
866	1req	A	396	482	1.80E-10	0.64	-0.19		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
866	1sig		386	463	1.80E-08	0.09	-0.19		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
871	1qgq	A	97	302	0.0018	0.06	0.22		SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN CHAIN: A;	TRANSFERASE GLYCOSYLTRANSFERASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
872	1b7f	A	6	104	1.40E-21	0.52	1		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*U P*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
872	1cvj	A	6	110	6.40E-24	0.52	0.92		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP *AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
872	1cvj	B	27	106	1.60E-20	0.99	1		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP *AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
872	1cvj	F	27	106	1.60E-20	0.92	1		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP *AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
872	1cvj	H	27	106	1.60E-20	0.95	1		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP *AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
872	1d8z	A	22	106	1.10E-21	0.83	1		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
872	1ha1		21	124	3.20E-22	0.48	1		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2
872	1sxl		24	109	1.40E-21	0.56	0.92		RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C- TERMINUS, OR SECOND	RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
872	2up1	A	19	124	1.30E-22	0.68	0.99		RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
872	3sxl	A	6	104	1.60E-20	0.58	0.99		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
873	1a4p	A	11	93	7.20E-18	0.66	1		S100A10; CHAIN: A, B;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN P11, CALPACTIN LIGHT CHAIN; S100 FAMILY, EF-HAND PROTEIN, LIGAND OF ANNEXIN II, 2 CALCIUM/PHOSPHOLIPID BINDING PROTEIN
873	1ap4		21	77	9.00E-07	-0.25	0.29		CARDIAC N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING CNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, CARDIAC MUSCLE 2 CONTRACTION
873	1bu3		22	78	5.40E-07	-0.05	0.15		CALCIUM-BINDING PROTEIN; CHAIN: NULL;	CALCIUM BINDING CALCIUM BINDING
873	1c7w	A	22	78	7.20E-07	-0.22	0.16		CALCIUM VECTOR PROTEIN; CHAIN: A;	METAL BINDING PROTEIN CAVP; EF-HAND FAMILY, CALCIUM BINDING PROTEIN, NMR
873	1cb1		8	83	9.00E-22	0.35	1		CALCIUM-BINDING PROTEIN CALBINDIN D9K (INTACT FORM) (NMR, 13 STRUCTURES) 1CB1 3	
873	1cll		11	92	3.60E-07	-0.14	0.16		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
873	1fpw	A	11	81	9.00E-08	-0.07	0.01		CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A;	METAL BINDING PROTEIN YEAST FREQUENIN EF-HAND, CALCIUM
873	1mr8	A	1	93	1.80E-17	0.15	0.81		MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8; CHAIN: A, B;	METAL TRANSPORT MRP8, S100A8, CALGRANULIN A CALCIUM-BINDING PROTEIN, CRYSTAL STRUCTURE, MAD, MIGRATION 2 INHIBITORY FACTOR_ RELATED PROTEIN 8, S100 PROTEIN
873	1qls	A	8	92	1.80E-18	0.38	1		S100C PROTEIN; CHAIN: A; ANNEXIN I; CHAIN: D;	COMPLEX (LIGAND/ANNEXIN) CALGIZZARIN; S100 FAMILY, EF-HAND PROTEIN, COMPLEX (LIGAND/ANNEXIN), 2 LIGAND OF ANNEXIN II, CALCIUM/PHOSPHOLIPID BINDING PROTEIN
874	1auk		39	330	9.60E-65	0.29	0.46		ARYLSULFATASE A; CHAIN: NULL;	HYDROLASE CEREBROSIDE-3-SULFATE-SULFATASE; CEREBROSIDE-3-SULFATE HYDROLYSIS, LYSOSOMAL ENZYME, 2 HYDROLASE
875	1dci	A	48	121	1.80E-14	-0.17	0.17		DIENOYL-COA ISOMERASE; CHAIN: A, B, C;	LYASE DELTA3,5,DELTA2,4-DIENOYL-COENZYME A ISOMERASE, LYASE, DIENOYL-COA ISOMERASE
875	1dci	A	55	144	3.20E-22	-0.02	0.35		DIENOYL-COA ISOMERASE; CHAIN: A, B, C;	LYASE DELTA3,5,DELTA2,4-DIENOYL-COENZYME A ISOMERASE, LYASE, DIENOYL-COA ISOMERASE
875	1ef8	A	45	145	1.60E-18	-0.23	0.01		METHYLMALONYL COA DECARBOXYLASE; CHAIN: A, B, C;	LYASE METHYLMALONYL COA, DECARBOXYLASE
875	1nzy	A	47	144	4.80E-21	0.3	-0.11		4-CHLORO BENZOYL COENZYME A DEHALOGENASE; CHAIN: A, B, C;	LYASE DEHALOGENASE; LYASE
875	2dub	A	47	144	3.20E-24	-0.11	0.13		2-ENOYL-COA HYDRATASE; CHAIN: A, B, C, D, E, F;	LYASE CROTONASE, ENOYL-COA HYDRATASE 1; LYASE, HYDRATASE, B-OXIDATION, FATTY ACID DEGRADATION, COA, 2 LIGAND BINDING

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
877	1ayz	A	1	151	3.60E-63			139.32	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
877	1ayz	A	2	146	3.60E-63	0.84	1		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
877	1qqq	A	1	147	9.00E-63			226.34	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
877	1qqq	A	2	147	9.00E-63	0.91	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
877	1qqq	A	3	146	4.80E-62	0.71	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
878	100E+96	B	12	137	3.20E-09	0.15	-0.14		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALING COMPLEX RAC1; P67PHOX; SIGNALING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
878	1elr	A	7	112	1.60E-18	0.31	-0.15		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
878	1elw	A	54	153	8.00E-09	0.02	-0.19		TPR1-DOMAIN OF HOP; CHAIN: A; B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
878	1fch	A	1	157	4.80E-14	0.04	-0.18		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
878	1fch	A	12	241	1.40E-23	0.01	-0.18		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
881	1ael	A	33	147	6.40E-29	0.35	1		TROPINONE REDUCTASE-I; CHAIN: A, B;	OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
881	lael	B	33	147	6.40E-29	0.36	1		TROPINONE REDUCTASE-I; CHAIN: A, B;	DEHYDROGENASE OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
881	lb16	A	38	129	1.40E-21	0.14	0.9		ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE OXIDOREDUCTASE, DETOXIFICATION, METABOLISM, ALCOHOL 2 DEHYDROGENASE, DROSOPHILA LEBANONENSIS, SHORT-CHAIN 3 DEHYDROGENASES/REDUCTASES, TERNARY COMPLEX, NAD-3- PENTANONE 4 ADDUCT
881	lbdb		36	147	1.60E-24	0.32	0.93		CIS-BIPHENYL-2,3- DIHYDRODIOL-2,3- DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE NAD-DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB DEGRADATION
881	leyd	A	36	148	4.80E-21	0.1	0.98		CARBONYL REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE
881	lfmc	A	31	147	1.60E-34	0.68	1		7 ALPHA- HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE/REDUCTASE, BILE ACID CATABOLISM
881	lhdc	A	35	148	1.10E-29	0.34	0.99		OXIDOREDUCTASE 3- ALPHA, 20-BETA- HYDROXYSTEROID DEHYDROGENASE (E.C.1.1.1.53) IHDC 3 COMPLEXED WITH CARBENOXOLONE IHDC 4	
881	loaa		38	129	1.80E-20	0.47	0.9		SEPIAPTERIN REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE SEPIAPTERIN REDUCTASE, TETRAHYDROBIOPTERIN, OXIDOREDUCTASE
881	lybv	A	23	147	4.80E-33	0.38	1		TRIHYDROXYNAPHTHALEN E REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE NAPHTHOL REDUCTASE; OXIDOREDUCTASE
881	2ae2	A	31	147	6.40E-29	0.49	0.99		TROPINONE REDUCTASE-II;	OXIDOREDUCTASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									CHAIN: A, B;	OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO PSEUDOTROPINE, SHORT-CHAIN DEHYDROGENASE
882	1ayz	A	6	157	1.10E-45	0.49	1		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
882	1ayz	A	6	171	1.10E-45			90.32	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
882	1c4z	D	10	157	6.40E-39	0.3	1		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
882	1c4z	D	10	166	6.40E-39			89.72	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
882	1qcq	A	7	168	9.60E-49			87.99	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
882	1qcq	A	8	157	9.60E-49	0.6	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
882	1u9a	A	3	168	9.60E-43			74.26	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2
882	1u9a	A	5	157	9.60E-43	0.17	1		UBC9; CHAIN: NULL;	PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
882	2aak		5	157	6.40E-48	0.38	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2
882	2aak		6	148	6.40E-48			93.12	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
882	2e2c		1	156	3.20E-44			81.53	UBIQUITIN CONJUGATING	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
882	2e2c		3	157	3.20E-44	0.27	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
882	2ucz		6	157	3.20E-51	0.63	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
882	2ucz		7	165	3.20E-51			121.4	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
882	1ayz	A	6	178	6.40E-50			114.6	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
882	1ayz	A	6	178	6.40E-50	0.73	1		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
882	1c4z	D	10	165	3.20E-42	0.4	1		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
882	1c4z	D	10	169	3.20E-42			104.56	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
882	1qcq	A	7	166	1.10E-53			104.4	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
882	1qcq	A	8	166	1.10E-53	0.53	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
882	1u9a	A	3	174	4.80E-45			94.76	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
882	1u9a	A	5	173	4.80E-45	0.8	1		UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
882	2aak		5	172	8.00E-52	0.62	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
882	2aak		6	174	8.00E-52			116.78	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
882	2e2c		1	176	1.60E-45			109.63	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
882	2e2c		3	160	1.60E-45	0.55	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
882	2ucz		6	160	1.60E-55	0.59	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
882	2ucz		7	174	1.60E-55			148.79	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE, YEAST
882	1ayz	A	6	128	4.80E-37	0.19	0.75		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION, LIGASE, YEAST
882	1c4z	D	10	128	1.60E-28	-0.22	0.54		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
882	1c4z	D	10	163	1.60E-28			51.09	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
882	1qcq	A	8	128	3.20E-39	0.2	0.6		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
882	1u9a	A	5	128	3.20E-34	-0.18	0.72		UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-DIRECTED 2
882	2aak		5	128	3.20E-38	0.06	0.55		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
882	2aak		6	155	3.20E-38			50.62	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
882	2e2c		3	126	1.10E-35	0.17	0.25		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
882	2ucz		6	128	1.60E-35	-0.09	0.49		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
882	2ucz		7	136	1.60E-35			56.09	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
883	1ayz	A	6	157	1.10E-45	0.49	1		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
883	1ayz	A	6	171	1.10E-45			90.32	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
883	1c4z	D	10	157	6.40E-39	0.3	1		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
883	1c4z	D	10	166	6.40E-39			89.72	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
883	1qcq	A	7	168	9.60E-49			87.99	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
883	1qcq	A	8	157	9.60E-49	0.6	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
883	1u9a	A	3	168	9.60E-43			74.26	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
883	1u9a	A	5	157	9.60E-43	0.17	1		UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
883	2aak		5	157	6.40E-48	0.38	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
883	2aak		6	148	6.40E-48			93.12	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
883	2e2c		1	156	3.20E-44			81.53	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
883	2e2c		3	157	3.20E-44	0.27	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
883	2ucz		6	157	3.20E-51	0.63	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
883	2ucz		7	165	3.20E-51			121.4	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
883	1ayz	A	6	178	6.40E-50			114.6	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
883	1ayz	A	6	178	6.40E-50	0.73	1		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
883	1c4z	D	10	165	3.20E-42	0.4	1		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
883	1c4z	D	10	169	3.20E-42			104.56	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
883	1qcq	A	7	166	1.10E-53			104.4	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
883	1qcq	A	8	166	1.10E-53	0.53	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
883	1u9a	A	3	174	4.80E-45			94.76	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-CONJUGATING ENZYME,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
883	1u9a	A	5	173	4.80E-45	0.8	1		UBC9; CHAIN: NULL;	UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
883	2aak		5	172	8.00E-52	0.62	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME
883	2aak		6	174	8.00E-52			116.78	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
883	2c2c		1	176	1.60E-45			109.63	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
883	2c2c		3	160	1.60E-45	0.55	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
883	2ucz		6	160	1.60E-55	0.59	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
883	2ucz		7	174	1.60E-55			148.79	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
883	1ayz	A	6	128	4.80E-37	0.19	0.75		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
883	1c4z	D	10	128	1.60E-28	-0.22	0.54		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
883	1c4z	D	10	163	1.60E-28			51.09	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
883	1qcq	A	8	128	3.20E-39	0.2	0.6		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST
883	1u9a	A	5	128	3.20E-34	-0.18	0.72		UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
										UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
883	2aak		5	128	3.20E-38	0.06	0.55		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1;
883	2aak		6	155	3.20E-38			50.62	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
883	2e2c		3	126	1.10E-35	0.17	0.25		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1;
									UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
883	2ucz		6	128	1.60E-35	-0.09	0.49		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7;
883	2ucz		7	136	1.60E-35			56.09	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE, YEAST
										UBIQUITIN CONJUGATION UBC7;
884	1ayz	A	6	157	1.10E-45	0.49	1		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION, LIGASE, YEAST
884	1ayz	A	6	171	1.10E-45			90.32	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2;
884	1c4z	D	10	157	6.40E-39	0.3	1		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	UBIQUITIN-CONJUGATING ENZYME
884	1c4z	D	10	166	6.40E-39			89.72	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
884	1qcq	A	7	168	9.60E-49			87.99	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
884	1qcq	A	8	157	9.60E-49	0.6	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
884	1u9a	A	3	168	9.60E-43			74.26	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME;

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
884	1u9a	A	5	157	9.60E-43	0.17	1		UBC9; CHAIN: NULL;	UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
884	2aak		5	157	6.40E-48	0.38	1			UBIQUITIN-CONJUGATING ENZYME
884	2aak		6	148	6.40E-48			93.12		UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
884	2e2c		1	156	3.20E-44			81.53		UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
884	2e2c		3	157	3.20E-44	0.27	1			UBIQUITIN CONJUGATING ENZYME; UBIQUITIN CONJUGATION, LIGASE
884	2ucz		6	157	3.20E-51	0.63	1			UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
884	2ucz		7	165	3.20E-51			121.4		UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
884	1ayz	A	6	178	6.40E-50			114.6		UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
884	1ayz	A	6	178	6.40E-50	0.73	1			UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
884	1c4z	D	10	165	3.20E-42	0.4	1			LIGASE E6AF; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3
884	1c4z	D	10	169	3.20E-42			104.56		UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
884	1qcq	A	7	166	1.10E-53			104.4	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
884	1qcq	A	8	166	1.10E-53	0.53	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
884	1u9a	A	3	174	4.80E-45			94.76	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
884	1u9a	A	5	173	4.80E-45	0.8	1		UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
884	2aak		5	172	8.00E-52	0.62	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1;
884	2aak		6	174	8.00E-52			116.78	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE
884	2e2c		1	176	1.60E-45			109.63	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, UBIQUITIN 2 BOND, LIGASE
884	2e2c		3	160	1.60E-45	0.55	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, UBIQUITIN 2 BOND, LIGASE
884	2ucz		6	160	1.60E-55	0.59	1		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; YEAST
884	2ucz		7	174	1.60E-55			148.79	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
884	1ayz	A	6	128	4.80E-37	0.19	0.75		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
884	1c4z	D	10	128	1.60E-28	-0.22	0.54		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBC7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
884	1c4z	D	10	163	1.60E-28			51.09	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D; UBIQUITIN CONJUGATING ENZYME; CHAIN: A; UBC9; CHAIN: NULL;	LIGASE E6AP, UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
884	1qqq	A	8	128	3.20E-39	0.2	0.6			LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST
884	1u9a	A	5	128	3.20E-34	-0.18	0.72			UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
884	2aak		5	128	3.20E-38	0.06	0.55		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1;
884	2aak		6	155	3.20E-38			50.62	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1;
884	2e2c		3	126	1.10E-35	0.17	0.25		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
884	2ucz		6	128	1.60E-35	-0.09	0.49		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7;
884	2ucz		7	136	1.60E-35			56.09	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION, LIGASE, YEAST
885	1av1	A	237	427	5.40E-07			53.53	APOLIPOPROTEIN A-1; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-1; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
885	1ega	A	39	350	1.60E-37	-0.14	0.01		GTP-BINDING PROTEIN ERA; CHAIN: A, B;	HYDROLASE ERA, GTPASE, RNA-BINDING, RAS-LIKE, HYDROLASE
885	1g7s	A	45	289	6.40E-06	-0.34	0.03		TRANSLATION INITIATION FACTOR IF2/EIF5B; CHAIN: A;	TRANSLATION TRANSLATIONAL GTPASE
885	1quu	A	283	426	1.80E-08	0.23	-0.01		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
885	1quu	A	302	445	1.80E-08	0.23	-0.01		HUMAN SKELETAL MUSCLE	CONTRACTILE PROTEIN TRIPLE-

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
									ALPHA-ACTININ 2; CHAIN: A;	HELIX COILED COIL, CONTRACTILE PROTEIN
886	1avl	A	237	427	5.40E-07			53.53	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
886	1ega	A	39	350	1.60E-37	-0.14	0.01		GTP-BINDING PROTEIN ERA; CHAIN: A, B;	HYDROLASE ERA, GTPASE, RNA-BINDING, RAS-LIKE, HYDROLASE
886	1g7s	A	45	289	6.40E-06	-0.34	0.03		TRANSLATION INITIATION FACTOR IF2/EIF5B; CHAIN: A;	TRANSLATION TRANSLATIONAL GTPASE
886	1quu	A	283	426	1.80E-08	0.23	-0.01		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
886	1quu	A	302	445	1.80E-08	0.23	-0.01		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
887	1b6d	A	19	118	3.20E-41	0.2	0.17		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN
887	1bj1	L	19	116	3.20E-43	0.13	0.11		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
887	1bvk	A	19	119	1.60E-42	0.18	-0.09		HULYSL1; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
887	1bw w	A	19	118	4.80E-43	0.15	0.34		IG KAPPA CHAIN V-J REGION REI; CHAIN: A, B;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
887	1dee	A	19	115	3.20E-43	-0.2	-0.1		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENICE-JONES 2 PROTEIN, IMMUNE SYSTEM

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
887	1fgv	L	19	116	3.20E-44	0.31	0.13		BINDING PROTEIN A; CHAIN: G, H;	THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
887	1lgm	L	19	125	1.40E-42	0	-0.06		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 'H52' (HUH52-AA FV) IFGV 4	
887	1vge	L	22	118	6.40E-41	0.15	0.23		IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG- M) FV FRAGMENT IIGM 3 TR1.9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TR1.9, ANTI- THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
887	2fgw	L	19	116	1.60E-44	0.32	0.1		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
888	1bw 5		216	275	9.00E-31	0.14	0.42		INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN
888	1fjl	A	216	275	1.10E-28	0.28	1		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
888	1fjl	A	216	280	1.10E-28			76.5	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
888	1fjl	B	217	273	9.00E-28			72.69	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
888	1fjl	B	217	274	9.00E-28	0.02	1		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX,

SEQ ID NO:	PDB ID	Chain ID	Start AA	End AA	PSI-BLAST	Verify score	PMF score	SeqFold score	Compound	PDB annotation
888	1pdn	C	35	152	9.60E-29	0.57	1		PRD PAIRED DOMAIN; CHAIN: C; IPDN 4 DNA; CHAIN: A, B IPDN 5	TRANSCRIPTION 2 REGULATING COMPLEX (GENE REGULATING PROTEIN/DNA) PAX, PRD, PAIRED DOMAIN, DNA-BINDING PROTEIN IPDN 14
888	1pdn	C	35	160	1.10E-63			168.62	PRD PAIRED DOMAIN; CHAIN: C; IPDN 4 DNA; CHAIN: A, B IPDN 5	COMPLEX (GENE REGULATING PROTEIN/DNA) PAX, PRD, PAIRED DOMAIN, DNA-BINDING PROTEIN IPDN 14
888	1pdn	C	35	160	1.10E-63	0.66	1		PRD PAIRED DOMAIN; CHAIN: C; IPDN 4 DNA; CHAIN: A, B IPDN 5	COMPLEX (GENE REGULATING PROTEIN/DNA) PAX, PRD, PAIRED DOMAIN, DNA-BINDING PROTEIN IPDN 14
888	2lfb		209	280	1.40E-30	0.31	0.33		LFBI/HNF1 TRANSCRIPTION FACTOR; CHAIN: NULL;	DNA-BINDING DNA-BINDING, TRANSCRIPTION FACTOR, LFBI/HNF1, 2 HELIX-TURN-HELIX, DNA-BINDING DOMAIN
888	6pax	A	34	169	1.60E-67			143.36	HOMEBOX PROTEIN PAX- 6; CHAIN: A; 26 NUCLEOTIDE DNA; CHAIN: B; 26 NUCLEOTIDE DNA; CHAIN: C;	GENE REGULATION/DNA PAX, PAIRED DOMAIN, TRANSCRIPTION, PROTEIN-DNA INTERACTIONS, 2 GENE REGULATION/DNA
888	6pax	A	35	152	1.60E-31	0.61	1		HOMEBOX PROTEIN PAX- 6; CHAIN: A; 26 NUCLEOTIDE DNA; CHAIN: B; 26 NUCLEOTIDE DNA; CHAIN: C;	GENE REGULATION/DNA PAX, PAIRED DOMAIN, TRANSCRIPTION, PROTEIN-DNA INTERACTIONS, 2 GENE REGULATION/DNA
888	6pax	A	36	169	1.60E-67	0.48	1		HOMEBOX PROTEIN PAX- 6; CHAIN: A; 26 NUCLEOTIDE DNA; CHAIN: B; 26 NUCLEOTIDE DNA; CHAIN: C;	GENE REGULATION/DNA PAX, PAIRED DOMAIN, TRANSCRIPTION, PROTEIN-DNA INTERACTIONS, 2 GENE REGULATION/DNA

TABLE 6

SEQ ID NO:	Position of Last Amino Acid of Signal Peptide	Maximum Score	Mean Score
445	21	0.993	0.931
446	14	0.975	0.962
447	42	0.986	0.606
448	18	0.908	0.703
449	24	0.967	0.778
450	30	0.992	0.946
452	17	0.997	0.973
454	32	0.907	0.575
455	27	0.931	0.672
456	40	0.988	0.755
457	26	0.986	0.916
458	18	0.920	0.750
459	15	0.946	0.790
460	21	0.993	0.931
461	47	0.942	0.644
463	24	0.886	0.712
464	36	0.985	0.865
465	42	0.965	0.679
466	25	0.980	0.946
467	27	0.969	0.858
469	26	0.950	0.793
470	45	0.983	0.687
471	25	0.981	0.821
472	30	0.998	0.963
473	18	0.977	0.915
474	27	0.949	0.644
475	23	0.913	0.768
476	19	0.947	0.901
477	15	0.936	0.628
478	17	0.956	0.893
479	17	0.942	0.720
480	19	0.952	0.730
481	17	0.970	0.916
483	14	0.975	0.962
486	47	0.955	0.727
488	23	0.991	0.952
495	42	0.986	0.606
496	11	0.971	0.594
502	29	0.896	0.743
509	18	0.908	0.703
510	13	0.959	0.908
512	20	0.957	0.858
516	24	0.967	0.778
517	35	0.991	0.851
518	26	0.939	0.722
519	47	0.983	0.640
522	30	0.992	0.946
538	16	0.974	0.924
550	17	0.997	0.973
551	42	0.947	0.588
555	30	0.981	0.684
576	32	0.907	0.575
577	26	0.973	0.927
578	27	0.931	0.672
589	40	0.988	0.755
590	38	0.985	0.775

595	20	0.938	0.818
611	18	0.920	0.750
615	25	0.949	0.775
616	33	0.995	0.835
617	15	0.946	0.790
623	19	0.921	0.819
627	21	0.993	0.931
634	20	0.961	0.674
635	28	0.954	0.648
645	47	0.942	0.644
647	31	0.962	0.776
650	16	0.949	0.782
651	14	0.963	0.613
654	20	0.984	0.958
670	24	0.886	0.712
673	17	0.934	0.753
678	36	0.985	0.865
695	23	0.954	0.754
707	42	0.965	0.679
708	2	0.979	0.667
709	24	0.984	0.851
710	17	0.911	0.745
717	25	0.980	0.946
718	35	0.988	0.871
726	27	0.969	0.858
730	17	0.981	0.844
741	22	0.937	0.871
755	17	0.890	0.668
764	26	0.950	0.793
768	32	0.958	0.827
771	45	0.983	0.687
773	39	0.997	0.801
776	17	0.945	0.650
787	32	0.983	0.835
789	25	0.981	0.821
792	31	0.966	0.815
796	22	0.887	0.572
797	19	0.941	0.691
807	30	0.998	0.963
808	18	0.977	0.915
809	18	0.977	0.915
811	27	0.959	0.827
812	16	0.925	0.734
815	19	0.934	0.564
816	21	0.960	0.858
818	27	0.949	0.644
821	27	0.943	0.758
823	27	0.908	0.728
833	23	0.913	0.768
837	19	0.947	0.901
841	22	0.967	0.826
845	15	0.936	0.628
846	20	0.975	0.840
851	31	0.985	0.908
852	19	0.965	0.922
853	39	0.984	0.743
857	17	0.956	0.893
858	21	0.957	0.868
861	22	0.975	0.866
868	21	0.942	0.736

871	43	0.973	0.560
873	19	0.952	0.730
874	33	0.923	0.717
879	23	0.978	0.911
881	16	0.947	0.884
887	17	0.970	0.916

TABLE 7

SEQ ID NO:	Position of Last Amino Acid of Signal Peptide	Maximum Score	Mean Score
445	21	0.993	0.931
446	14	0.975	0.962
447	42	0.986	0.606
448	18	0.908	0.703
449	24	0.967	0.778
450	30	0.992	0.946
452	17	0.997	0.973
454	32	0.907	0.575
455	27	0.931	0.672
456	40	0.988	0.755
457	26	0.986	0.916
458	18	0.920	0.750
459	15	0.946	0.790
460	21	0.993	0.931
461	47	0.942	0.644
463	24	0.886	0.712
464	36	0.985	0.865
465	42	0.965	0.679
466	25	0.980	0.946
467	27	0.969	0.858
469	26	0.950	0.793
470	45	0.983	0.687
471	25	0.981	0.821
472	30	0.998	0.963
473	18	0.977	0.915
474	27	0.949	0.644
475	23	0.913	0.768
476	19	0.947	0.901
477	15	0.936	0.628
478	17	0.956	0.893
479	17	0.942	0.720
480	19	0.952	0.730
481	17	0.970	0.916
483	14	0.975	0.962
486	47	0.955	0.727
488	23	0.991	0.952
495	42	0.986	0.606
496	11	0.971	0.594
502	29	0.896	0.743
509	18	0.908	0.703
510	13	0.959	0.908
512	20	0.957	0.858
516	24	0.967	0.778
517	35	0.991	0.851
518	26	0.939	0.722
519	47	0.983	0.640
522	30	0.992	0.946
538	16	0.974	0.924
550	17	0.997	0.973
551	42	0.947	0.588
555	30	0.981	0.684
576	32	0.907	0.575
577	26	0.973	0.927
578	27	0.931	0.672
589	40	0.988	0.755

590	38	0.985	0.775
595	20	0.938	0.818
611	18	0.920	0.750
615	25	0.949	0.775
616	33	0.995	0.835
617	15	0.946	0.790
623	19	0.921	0.819
627	21	0.993	0.931
634	20	0.961	0.674
635	28	0.954	0.648
645	47	0.942	0.644
647	31	0.962	0.776
650	16	0.949	0.782
651	14	0.963	0.613
654	20	0.984	0.958
670	24	0.886	0.712
673	17	0.934	0.753
678	36	0.985	0.865
695	23	0.954	0.754
707	42	0.965	0.679
708	2	0.979	0.667
709	24	0.984	0.851
710	17	0.911	0.745
717	25	0.980	0.946
718	35	0.988	0.871
726	27	0.969	0.858
730	17	0.981	0.844
741	22	0.937	0.871
755	17	0.890	0.668
764	26	0.950	0.793
768	32	0.958	0.827
771	45	0.983	0.687
773	39	0.997	0.801
776	17	0.945	0.650
787	32	0.983	0.835
789	25	0.981	0.821
792	31	0.966	0.815
796	22	0.887	0.572
797	19	0.941	0.691
807	30	0.998	0.963
808	18	0.977	0.915
809	18	0.977	0.915
811	27	0.959	0.827
812	16	0.925	0.734
815	19	0.934	0.564
816	21	0.960	0.858
818	27	0.949	0.644
821	27	0.943	0.758
823	27	0.908	0.728
833	23	0.913	0.768
837	19	0.947	0.901
841	22	0.967	0.826
845	15	0.936	0.628
846	20	0.975	0.840
851	31	0.985	0.908
852	19	0.965	0.922
853	39	0.984	0.743
857	17	0.956	0.893
858	21	0.957	0.868
861	22	0.975	0.866

868	21	0.942	0.736
871	43	0.973	0.560
873	19	0.952	0.730
874	33	0.923	0.717
879	23	0.978	0.911
881	16	0.947	0.884
887	17	0.970	0.916

TABLE 8

SEQ ID NO: of Nucleotide Sequence	SEQ ID NO: of Polypeptide Sequence	SEQ ID NO: in USSN 09/659,671
1	445	2
2	446	5
3	447	6
4	448	7
5	449	8
6	450	9
7	451	11
8	452	12
9	453	13
10	454	14
11	455	15
12	456	16
13	457	17
14	458	18
15	459	19
16	460	20
17	461	21
18	462	23
19	463	24
20	464	25
21	465	28
22	466	29
23	467	30
24	468	31
25	469	34
26	470	35
27	471	37
28	472	38
29	473	39
30	474	40
31	475	41
32	476	42
33	477	43
34	478	44
35	479	45
36	480	46
37	481	47
38	482	49
39	483	50
40	484	51
41	485	52
42	486	53
43	487	54
44	488	55
45	489	56
46	490	57
47	491	58
48	492	59
49	493	60
50	494	61
51	495	62
52	496	63
53	497	64
54	498	65

55	499	66
56	500	67
57	501	68
58	502	69
59	503	70
60	504	71
61	505	72
62	506	73
63	507	74
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81	525	94
82	526	95
83	527	96
84	528	97
85	529	98
86	530	99
87	531	100
88	532	101
89	533	102
90	534	105
91	535	106
92	536	107
93	537	108
94	538	109
95	539	110
96	540	111
97	541	112
98	542	113
99	543	114
100	544	115
101	545	116
102	546	117
103	547	118
104	548	119
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107	551	122
108	552	123
109	553	124
110	554	125
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112	556	127
113	557	128
114	558	129

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120	564	135
121	565	136
122	566	137
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126	570	141
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132	576	147
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134	578	150
135	579	151
136	580	152
137	581	153
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166	610	183
167	611	184
168	612	185
169	613	186
170	614	187
171	615	188
172	616	189
173	617	190
174	618	191

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176	620	193
177	621	194
178	622	195
179	623	197
180	624	198
181	625	199
182	626	200
183	627	201
184	628	202
185	629	203
186	630	204
187	631	205
188	632	206
189	633	207
190	634	208
191	635	209
192	636	210
193	637	211
194	638	212
195	639	213
196	640	214
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199	643	217
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205	649	223
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213	657	232
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216	660	235
217	661	236
218	662	237
219	663	238
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221	665	240
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224	668	243
225	669	244
226	670	245
227	671	246
228	672	247
229	673	248
230	674	249
231	675	250
232	676	251
233	677	252
234	678	253

235	679	254
236	680	255
237	681	256
238	682	258
239	683	259
240	684	260
241	685	261
242	686	262
243	687	263
244	688	264
245	689	265
246	690	266
247	691	267
248	692	268
249	693	269
250	694	270
251	695	271
252	696	272
253	697	273
254	698	274
255	699	275
256	700	277
257	701	278
258	702	279
259	703	280
260	704	282
261	705	283
262	706	284
263	707	285
264	708	286
265	709	287
266	710	288
267	711	289
268	712	290
269	713	291
270	714	292
271	715	293
272	716	294
273	717	295
274	718	296
275	719	297
276	720	298
277	721	299
278	722	300
279	723	301
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281	725	304
282	726	305
283	727	306
284	728	307
285	729	308
286	730	309
287	731	310
288	732	311
289	733	312
290	734	313
291	735	314
292	736	316
293	737	317
294	738	318

295	739	319
296	740	320
297	741	321
298	742	322
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300	744	324
301	745	325
302	746	326
303	747	327
304	748	328
305	749	329
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307	751	331
308	752	332
309	753	333
310	754	334
311	755	335
312	756	336
313	757	337
314	758	338
315	759	339
316	760	340
317	761	341
318	762	342
319	763	343
320	764	344
321	765	345
322	766	346
323	767	347
324	768	348
325	769	349
326	770	350
327	771	351
328	772	352
329	773	353
330	774	354
331	775	355
332	776	356
333	777	357
334	778	358
335	779	359
336	780	360
337	781	361
338	782	362
339	783	363
340	784	364
341	785	366
342	786	367
343	787	368
344	788	369
345	789	370
346	790	371
347	791	372
348	792	373
349	793	374
350	794	376
351	795	377
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353	797	379
354	798	380

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357	801	383
358	802	384
359	803	385
360	804	386
361	805	387
362	806	388
363	807	389
364	808	390
365	809	391
366	810	392
367	811	393
368	812	395
369	813	396
370	814	397
371	815	398
372	816	399
373	817	400
374	818	401
375	819	402
376	820	403
377	821	404
378	822	406
379	823	407
380	824	408
381	825	409
382	826	410
383	827	411
384	828	412
385	829	413
386	830	414
387	831	416
388	832	417
389	833	418
390	834	419
391	835	420
392	836	421
393	837	422
394	838	423
395	839	424
396	840	425
397	841	426
398	842	427
399	843	428
400	844	429
401	845	430
402	846	431
403	847	432
404	848	433
405	849	435
406	850	436
407	851	437
408	852	438
409	853	439
410	854	440
411	855	441
412	856	442
413	857	443
414	858	445

415	859	446
416	860	447
417	861	448
418	862	449
419	863	450
420	864	451
421	865	452
422	866	453
423	867	454
424	868	455
425	869	456
426	870	457
427	871	458
428	872	459
429	873	460
430	874	461
431	875	462
432	876	463
433	877	464
434	878	465
435	879	466
436	880	467
437	881	468
438	882	469
439	883	470
440	884	471
441	885	472
442	886	473
443	887	474
444	888	475

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-444, a mature protein coding portion of SEQ ID NO: 1-444, an active domain coding portion of SEQ ID NO: 1-444, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1;
and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-444.

11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
 - a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
 - a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
 - a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
 - a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
 - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
 - b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from SEQ ID NO: 1-444, a mature protein coding portion of SEQ ID NO: 1-444, an active domain coding portion of SEQ ID NO: 1-444, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-444, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).
20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO: 217-432, or 649-864, the mature protein portion thereof, or the active domain thereof.
21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-444.
23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.